

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 15:09:16 ; Search time 35 Seconds
(without alignments)

45.686 Million cell updates/sec

Title: US-09-846-347-1
Perfect score: 64
Sequence: 1 DAHKSEVHRPK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : A_Geneseq_10.002:*

1:	/SID52/gcdata/geneseq/geneseq-emb1/AA1980.DAT:*	11	64	100.0	137	22	AA012088	Human polypeptide
2:	/SID52/gcdata/geneseq/geneseq-emb1/AA1981.DAT:*	12	64	100.0	192	22	AAU29875	Novel human secret
3:	/SID52/gcdata/geneseq/geneseq-emb1/AA1982.DAT:*	13	64	100.0	195	23	AA017048	Human serum albumi
4:	/SID52/gcdata/geneseq/geneseq-emb1/AA1983.DAT:*	14	64	100.0	204	21	AAU28937	Yeast codon-biased
5:	/SID52/gcdata/geneseq/geneseq-emb1/AA1984.DAT:*	15	64	100.0	214	22	AAU29874	Novel human secret
6:	/SID52/gcdata/geneseq/geneseq-emb1/AA1985.DAT:*	16	64	100.0	236	23	AA017051	Human albumin-thro
7:	/SID52/gcdata/geneseq/geneseq-emb1/AA1986.DAT:*	17	64	100.0	241	23	AA016984	Alpha-MSH construc
8:	/SID52/gcdata/geneseq/geneseq-emb1/AA1987.DAT:*	18	64	100.0	242	23	AA016985	Alpha-MSH construc
9:	/SID52/gcdata/geneseq/geneseq-emb1/AA1988.DAT:*	19	64	100.0	244	23	AA016986	Alpha-MSH construc
10:	/SID52/gcdata/geneseq/geneseq-emb1/AA1989.DAT:*	20	64	100.0	245	23	AA016987	Alpha-MSH construc
11:	/SID52/gcdata/geneseq/geneseq-emb1/AA1990.DAT:*	21	64	100.0	245	23	AA016988	Alpha-MSH construc
12:	/SID52/gcdata/geneseq/geneseq-emb1/AA1991.DAT:*	22	64	100.0	268	23	AA016989	Novel human secret
13:	/SID52/gcdata/geneseq/geneseq-emb1/AA1992.DAT:*	23	64	100.0	289	22	AAU29575	Novel human secret
14:	/SID52/gcdata/geneseq/geneseq-emb1/AA1993.DAT:*	24	64	100.0	301	22	AAU29876	Novel human secret
15:	/SID52/gcdata/geneseq/geneseq-emb1/AA1994.DAT:*	25	64	100.0	303	12	AAU29878	Human serum albumi
16:	/SID52/gcdata/geneseq/geneseq-emb1/AA1995.DAT:*	26	64	100.0	373	10	AAU90387	N-terminal of huma
17:	/SID52/gcdata/geneseq/geneseq-emb1/AA1996.DAT:*	27	64	100.0	388	10	AAU90389	N-terminal human s
18:	/SID52/gcdata/geneseq/geneseq-emb1/AA1997.DAT:*	28	64	100.0	389	10	AAU90388	N-terminal human s
19:	/SID52/gcdata/geneseq/geneseq-emb1/AA1998.DAT:*	29	64	100.0	390	10	AAU90391	N-terminal human s
20:	/SID52/gcdata/geneseq/geneseq-emb1/AA2000.DAT:*	30	64	100.0	401	22	AAU29876	Novel human secret
21:	/SID52/gcdata/geneseq/geneseq-emb1/AA2001.DAT:*	31	64	100.0	407	10	AAU90392	Novel human secret
22:	/SID52/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*	32	64	100.0	550	22	AAU29877	N-terminal human s
23:	/SID52/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*	33	64	100.0	585	10	AAU93344	Sequence of mature
		34	64	100.0	585	10	AAU93344	Mature human serum
		35	64	100.0	585	10	AAU91422	Human normal serum
		36	64	100.0	585	11	AAU05318	Human serum albumi
		37	64	100.0	585	11	AAU20209	Human serum albumi
		38	64	100.0	585	13	AAU26207	Human serum albumi
		39	64	100.0	585	13	AAU26362	Synthetic HSA prot
		40	64	100.0	585	13	AAU90388	Human serum albumi
		41	64	100.0	585	15	AAU80301	Human serum albumi
		42	64	100.0	585	18	AAU20111	HSA protein sequen
		43	64	100.0	585	19	AAU59845	Mature protein of
		44	64	100.0	585	21	AAU84873	Amino acid sequenc
		45	64	100.0	585	21	AAU83946	Yeast codon-biased
		46	64	100.0	585	21	ABR7906	Human mature biased
		47	64	100.0	585	22	AAE13311	Human albumin (HA)
		48	64	100.0	585	22	AAE13399	Human albumin (HA)
		49	64	100.0	585	22	AAE20111	Mature human serum
		50	64	100.0	585	22	AAE13129	Human albumin (HA)
		51	64	100.0	585	22	AAE13135	Human albumin (HA)
		52	64	100.0	585	22	AAE12403	Human albumin (HA)
		53	64	100.0	585	22	AAE12417	Human albumin (HA)
		54	64	100.0	585	22	AAE0578	Human serum albumi
		55	64	100.0	585	23	AAE63321	Human serum albumi
		56	64	100.0	585	23	ABU0986	B lymphocyte stimu
		57	64	100.0	585	23	ABG33847	Human B Lymphocyte
		58	64	100.0	585	23	ABU75220	Mature form of hum
		59	64	100.0	585	7	AAU60072	Sequence of human
		60	64	100.0	586	7	AAU60839	Sequence of human
		61	64	100.0	586	8	AAU70676	Human serum albumi
		62	64	100.0	588	12	AAU13021	B lymphocyte stimu
		63	64	100.0	590	12	AAU12558	Human B Lymphocyte
		64	64	100.0	590	12	AAU12559	Mature form of hum
		65	64	100.0	586	7	AAU60072	Sequence of human
		66	64	100.0	608	11	AAU05784	Sequence of human
		67	64	100.0	608	11	AAU04223	Human serum albumi
		68	64	100.0	609	4	AAU30089	HSA-fibronectin ce
		69	64	100.0	609	4	AAU30188	HSA-nuclear transi
		70	64	100.0	609	7	AAU0064	Fragmnet of plasmi
		71	64	100.0	609	7	AAU60092	Sequence of pre-pr
		72	64	100.0	609	13	AAU25309	Sequence of pre-pr
		73	64	100.0	609	13	AAU27860	Sequence encoded b
		74	64	100.0	609	14	AAU32563	Sequence of human
		75	64	100.0	609	17	AAU96232	Sequence of human
							ALIGNMENTS	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	64	100.0	12	22	ABT74367
2	64	100.0	12	22	ABT74370
3	64	100.0	20	21	AB12462
4	64	100.0	113	22	AB011631
5	64	100.0	116	22	AB002642
6	64	100.0	119	22	AB011632
7	64	100.0	123	22	AB004424
8	64	100.0	124	22	AB002630
9	64	100.0	133	4	ABP3004
10	64	100.0	133	22	AAU29925

RESULT 1
ID AAB74367 standard; peptide; 12 AA.
Novel human Secret

XX
 PS Example; Fig 1; 11PP; Japanese.
 XX
 CC The present invention describes hybridoma cells used for preparing an immunoglobulin G (IgG) monoclonal antibody capable of rapid reaction with human albumin. The hybridoma cells are prepared by fusion of mammal myeloma cells and spleen cells immunised with human serum albumin, and producing IgG monoclonal antibody which rapidly react with human albumin. The monoclonal antibodies can be used in the diagnosis of diabetic nephropathy. The present sequence represents a human albumin epitope peptide sequence which is used in an example from the present invention.
 CC
 CC invention.
 XX Sequence 20 AA;
 SQ Query Match 100.0%; Score 64; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0;
 DB 1 DAHKSEVAHRFK 12
 2 DAHKSEVAHRFK 13

RESULT 4
 AA011631
 ID AA011631 standard; Protein; 113 AA.
 XX
 AC AA011631;
 XX DT 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 2523.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 OS Homo Sapiens.
 XX PN WO200164835-A2.
 PD 07-SEP-2001.
 XX PF 26-FEB-2001; 2001WO-US04927.
 XX PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX PA (HYSE-) HYSEQ INC.
 PT Tang YT, Liu C, Drmanac RT;
 XX DR N-PSDB; AA182573.
 XX PT Isolated nucleic acids and polypeptides useful for preventing PT diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
 XX PS Claim 20; SEQ ID NO 16534; 1399pp + sequence Listing; English.
 XX The invention relates to human polynucleotides (AA19941-AA193841) and the encoded proteins (AA00100-AA013910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC Sequence 113 AA;
 SQ Query Match 100.0%; Score 64; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0;
 OY 1 DAHKSEVAHRFK 12
 DB 29 DAHKSEVAHRFK 40

RESULT 5
 AA02642
 ID AA02642 standard; Protein; 116 AA.
 XX AC AA02642;
 XX DT 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 16534.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200164835-A2.
 PD 07-SEP-2001.
 XX PR 26-FEB-2001; 2001WO-US04927.
 XX PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX PA (HYSE-) HYSEQ INC.
 XX PT Tang YT, Liu C, Drmanac RT;
 XX DR N-PSDB; AA182573.
 XX PT Isolated nucleic acids and polypeptides useful for preventing PT diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
 XX PS Claim 20; SEQ ID NO 16534; 1399pp + sequence Listing; English.
 XX The invention relates to human polynucleotides (AA19941-AA193841) and the encoded proteins (AA00100-AA013910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC Sequence 116 AA;
 SQ Query Match 100.0%; Score 64; DB 22; Length 116;

			Best Local Similarity	100.0%	Pred.	NO. 0.0018;			
Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Y	1	DAHKSEVAHRFK	12						
b	22	DAHKSEVAHRFK	33						
			RESULT 6						
AQ01632	D	AA01632	Standard; Protein; 119 AA.						
	X	X							
C	X	X							
	X	X							
T	X	X							
K	X	X							
S	X	X							
Homo sapiens.									
			Human polypeptide SEQ ID NO 25524.						
			Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; nervous system disorders; arthritis; inflammation.						
			Human; cytokine; cell proliferation; cell differentiation; gene therapy; tissue growth factor; immunomodulatory; cancer; Leukaemia; nervous system disorders; arthritis; inflammation.						
			(Homo sapiens).						
			WO200164835-A2.						
			07-SEP-2001.						
			26-FEB-2001; 2001WO-US04927.						
			28-FEB-2000; 2000US-0515126.						
			18-MAY-2000; 2000US-0577409.						
			(HYSE-) HYSEQ INC.						
			Tang YT, Liu C, Drmanac RT;						
			WPI; 2001-514838/56.						
			N-PSDB; AAI84355.						
			Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -						
			Claim 20; SEQ ID NO 18316; 1399pp + Sequence Listing; English.						
			The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA01910) that exhibit activity eliciting to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.						
			Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .						
			Sequence 119 AA;						
			Query Match Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
			RESULT 8						
			ID AAC02630 AAC02630 standard; Protein; 124 AA.						
			AC AAC02630; XX						
			DT 06-NOV-2001 (first entry)						
			XX						
			XX Human polypeptide SEQ ID NO 18316.						
			XX PD 07-SEP-2001.						
			XX 26-FEB-2001; 2001WO-US04927.						
			XX 28-FEB-2000; 2000US-0515126.						
			XX 18-MAY-2000; 2000US-0577409.						
			XX PA (HYSE-) HYSEQ INC.						
			XX PI Tang YT, Liu C, Drmanac RT;						
			XX DR WPI; 2001-514838/56.						
			XX N-PSDB; AAI84355.						
			XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -						
			XX PT Claim 20; SEQ ID NO 18316; 1399pp + Sequence Listing; English.						
			XX The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA01910) that exhibit activity eliciting to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.						
			CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .						
			CC Sequence 123 AA;						
			CC Query Match Best Local Similarity 100.0%; Pred. No. 0.0019; Length 123; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
			OY 1 DAHKSEVAHRFK 12						
			Db 23 DAHKSEVAHRFK 34						
			XX						

DE Human polypeptide SEQ ID NO 16522.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens

XX WO200104835-A2.

XX PD 07-SEP-2001.

XX PP 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

HYSEQ INC.

Yang YT, Liu C, Drmanac RT;

XX DR WIPI; 2001-514838/56.

DR N-PSSB; AAIB2561.

PT Isolated nucleic acids and polypeptides, useful for preventing

PT diagnosing and treating e.g. leukaemia, inflammation and immune

PT disorders -

PS Claim 20; SEQ ID NO 16522; 1399pp + Sequence Listing; English.

XX The invention relates to human Polynucleotides (AAI7941-AAI9381) and

CC the encoded proteins (AN0010-AN013910) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haemopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activating/inhibiting activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation.

Note: The sequence data for this patent did not form part of the printed

specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published_pct_sequence.

SQ Sequence 124 AA;

Query Match 100.0%; Score 64; DB 22; Length 124;

Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 DAHKSEVAHRPK 12

Oy 1 DAHKSEVAHRPK 12

XX

Qy 21 DAHKSEVAHRPK 32

Oy 27 DAHKSEVAHRPK 38

RESULT 9

AAP3004 ID AAP3004 standard; Protein; 133 AA.

AC AAP3004;

XX DT 25-APR-1992 (first entry)

XX Sequence encoded by recombinant DNA molecule pKT218(HSA/33-1 (BgIII-ECRI)-HSA/1'-3(BgIII-ECRI) human proserum albumin (except for the missing 36 nucleotide BgIII-BgIII deletion).

DB DE Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

DE Human; cytokeratin; blood; protein; nitrogen fixation; food additive; kermitcerus therapy.

KW Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PP 16-APR-2001; 2001WO-US08656.

XX Key Location/Qualifiers

XX FT Key 1..26

XX FT /label= signal

XX FT Protein 27..59

XX FT Protein /label= residues 1-33

XX FT Protein 60..92

XX FT Protein /label= residues 319-351

XX FT Protein 93..124

XX FT Protein /label= residues 368-399

XX FT Protein 125..133

XX FT Protein /label= residues 572-580

XX PN RP91527-A.

XX PD 19-OCT-1983.

XX PR 19-MAY-1983; 83EP-0200712.

XX PR 14-DEC-1981; 81US-0330912.

XX PA (HARD) HARVARD COLLEGE.

XX PI Gilbert W, Philipp BW;

XX DR WIPI; 1983-796530/43.

XX DR N-PSSB; AN30009.

XX PT Prodn. of human serum albumin-like polypeptide(s) - from host

XX PT transformed with recombinant DNA molecule

XX PS Example; Fig 4; 42pp; English.

XX AN3009 was prep'd. from two clones isolated from a human fetal liver

CC cDNA library screened with mouse serum albumin cDNA. The two clones

CC are pKT218(HSA/33-1) and pKT218(HSA/17-3), which were recombinant to

CC give AN3009, the coding sequence of which is out of phase by a

CC single nucleotide (Bee FT). However, as a result of perhaps some

CC internal start, host transformed with the hybrid gene (even out of

CC phase) in pKT218 still produce HSA-like products.

SQ Sequence 133 AA;

Query Match 100.0%; Score 64; DB 4; Length 133;

Best Local Similarity 100.0%; Pred. No. 0.00021; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 DAHKSEVAHRPK 12

Db 27 DAHKSEVAHRPK 38

RESULT 10

AAU29925 ID AAU29925 standard; Protein; 133 AA.

AC AAU29925;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #416.

XX Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PP 16-APR-2001; 2001WO-US08656.

CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haemopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. ARK29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

SQ Sequence 192 AA;
 Query Match 100.0%; Score 64; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; MisMatch 0; OS DE Human serum albumin (1-195) SEQ ID NO: 56.
 ID DAHKSEVAHRFK 12
 Db 53 DAHKSEVAHRFK 64
 RESUME 13
 AAO17048
 XX AA017048 standard; Protein: 195 AA.
 AC AAO17048;
 XX DT 29-MAY-2002 (first entry)
 XX OS DE Human serum albumin (1-195) SEQ ID NO: 56.
 KW Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; anti-inflammatory; anti-rheumatic;
 KW antiarthritic; antidiabetic; antimicrobial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 XX OS Homo sapiens.
 N WO200206316-A2.
 XX PD 24-JAN-2002.
 XX PP 16-JUL-2001; 2001WO-US222263.
 PR 14-JUL-2000; 2000US21831P.
 PR 18-AUG-2000; 2000US22682P.
 PR 06-OCT-2000; 2000US238310P.
 PR 29-DEC-2000; 2000US25874P.
 PR 14-JUN-2001; 2001US229317P.
 PA (ZYCO-) ZYROS INC.
 XX PI Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 XX DR WPI; 2002-195801/25.
 PT Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 PT stimulating hormone concatamer or its analog, for treating inflammatory
 PT or autoimmune disorders -
 PS Example 2; Page 46; 89pp; English.
 CC The present invention relates to a nucleic acid comprising a sequence

CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a protein described in the exemplification of the
 CC invention.
 SQ Sequence 195 AA;
 Query Match 100.0%; Score 64; DB 23; Length 195;
 Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; MisMatch 0; OS DE Human serum albumin (1-195) SEQ ID NO: 56.
 ID DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12
 RESULT 14
 ID AAY83947
 AC AAY83947 standard; Protein: 204 AA.
 XX DT AAY83947 (first entry)
 XX DB Yeast codon-biased recombinant HSA protein fragment HSA-I.
 KW Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
 KW overlapping oligonucleotide; expression vector.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN CN1239113-A.
 XX PD 22-DEC-1999.
 XX PF 17-JUN-1998; 98CN-0102506.
 XX PR 17-JUN-1998; 98CN-0102506.
 XX PA (HAIJ-) HAIJI BIOENGINEERING CO LTD.
 XX PI Li S, Lu D;
 XX DR WPI; 2000-351198/31.
 DR N-PSDB; AAA10092.
 XX PT Process for preparing recombinant human serum albumin - which comprises
 PT yeast biased sex codons
 XX Example 1; Fig 3; 44pp; Chinese.
 XX PR The method relates to a method of recombinantly producing human serum
 CC albumin (HSA) in yeast by altering the coding sequence of HSA to
 CC comprise a yeast codon bias. The complete HSA gene (AA10091) was
 CC generated as three synthetic fragments (AA10092-11094) joined by
 CC recombinant DNA technology. Each HSA fragment was synthesised from
 CC overlapping oligonucleotide fragments that were extended. This sequence
 CC represents the sequence of the HSA fragment HSA-I encoded by the human
 CC gene with a yeast codon bias. The invention also covers recombinant
 CC expression vector, yeast host cells carrying the recombinant expression
 CC vector and the process for producing human serum albumin in the yeast
 CC host cell, especially in secretory mode.
 SQ Sequence 204 AA;
 Query Match 100.0%; Score 64; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.00034; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ID AAU29874 standard; Protein; 214 AA.
 XX
 Db 8 DAHKSEVAHRFK 19

RESULT 15

ID AAU29874 standard; Protein; 214 AA.
 XX
 AC AAU29874;
 DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein #1365.

XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haemopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.

XX
 PF 16-APR-2001; 2001WO-US088656.

XX
 PR 18-APR-2000; 2000US-0552829.
 PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

XX
 PT Tang YT, Liu C, Drmanac RT;
 DR XX
 WPI; 2001-611725/70.

XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

XX
 PS Claim 20; Page 205; 765pp; English.

XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haemopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 214 AA;

Query Match 100.0%; Score 64; DB 22; Length 214;
 Best Local Similarity 100.0%; Prod. No. 0.00036; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ID AAU29874 standard; Protein; 241 AA.
 XX
 AC AAU29874;
 XX
 Db 37 DAHKSEVAHRFK 48

AM017051
 ID AA017051 standard; Protein; 236 AA.
 XX
 AC AA017051;
 XX
 DT 29-MAY-2002 (first entry)

XX
 DE Human albumin-thrombin-alpha-MSH SEQ ID NO: 82.

XX
 PN WO200206316-A2.

XX
 PD 24-JAN-2002.

XX
 PF 16-JUL-2001; 2001WO-US222263.

XX
 PR 14-JUL-2000; 2000US-21881P.
 PR 18-AUG-2000; 2000US-226382P.
 PR 06-OCT-2000; 2000US-238380P.
 PR 29-DEC-2000; 2000US-255764P.
 PR 14-JUN-2001; 2001US-288317P.

XX
 PA (ZYCO-) ZYCOS INC.

XX
 PT Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 DR XX
 WPI; 2002-195801/25.

XX
 PT Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 PT stimulating hormone concatamer or its analog, for treating inflammatory
 PT or autoimmune disorders -

XX
 PS Example 2; Page 48; 80pp; English.

XX
 CC The present invention relates to a nucleic acid comprising a sequence
 CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g. inflammatory disorder, or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a peptide described in the exemplification of the
 CC invention.

XX
 SQ Sequence 236 AA;

Query Match 100.0%; Score 64; DB 23; Length 236;
 Best Local Similarity 100.0%; Prod. No. 0.0004; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ID AA016984 standard; Protein; 241 AA.
 XX
 AC AA016984;
 XX
 Db 25 DAHKSEVAHRFK 36

XX
 DT 29-MAY-2002 (first entry)

XX DR DR
 XX PT DR
 XX PT stimulating hormone concatamer or its analog, for treating inflammatory
 XX PT or autoimmune disorders -
 XX
Disclosure: Page 5; 89pp; English.
 XX
 CC The present invention relates to a nucleic acid comprising a sequence
 CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g., inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a protein described in the exemplification of the
 CC invention.
 XX
Sequence 245 AA:
 Query Match 100.0%; Score 64; DB 23; Length 245;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 DAHKSEVAHRFK 12
 Db 25 DAHKSEVAHRFK 36
 XX
RESULT 22
 AAO16989
 ID AAO16989 Standard; Protein; 268 AA.
 XX
 AC AAO16989;
 XX
 DT 29-MAY-2002 (first entry)
 DE Alpha-MSH construct protein fragment SEQ ID NO: 60.
 DE Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoïd arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
 KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 KS Unidentified.
 XX
 DN WO200206316-A2.
 XX
 PD 24-JAN-2002.
 XX
 PP 16-JUL-2001; 2001WO-US22263.
 PR 14-JUL-2000; 2000US-218381P.
 PR 18-AUG-2000; 2000US-226382P.
 PR 06-OCT-2000; 2000US-238380P.
 PR 29-DEC-2000; 2000US-258764P.
 PR 14-JUN-2001; 2001US-29831TP.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 XX
 DR WPI; 2002-195801/25.
 XX
 PR Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 PR stimulating hormone concatamer or its analog, for treating inflammatory
 PR or autoimmune disorders -
 Example 2; Page 5; 89pp; English.

XX	CC	The present invention relates to a nucleic acid comprising a sequence encoding a fusion polypeptide having an alpha-melanocyte stimulating hormone (MSH) concatamer. The sequences are useful for treating an individual suffering from, or at risk of, a disorder of the immune system e.g. inflammatory disorder or autoimmune disorder, including rheumatoid arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact hypersensitivity, inflammatory bowel disease, autoimmune encephalitis, multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The present sequence is a protein described in the exemplification of the invention.
XX	CC	SQ Sequence 268 AA;
XX	CC	Query Match 100.0%; Score 64; DB 23; Length 268; Best Local Similarity 100.0%; Pred. No. 0.00046; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	CC	Qy 1 DAHKSEVAHRPK 12
XX	CC	Db 25 DAHKSEVAHRPK 36
XX	CC	RESULT 23
XX	CC	AAU29575 ID AAU29575 standard; Protein; 289 AA.
XX	CC	AC AAU29575;
XX	CC	DT 18-DEC-2001 (first entry)
XX	CC	DB Novel human secreted protein #66.
XX	CC	KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haemopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia; Homo sapiens.
XX	CC	OS Homo sapiens.
XX	CC	PN WO200179449-A2.
XX	CC	PD 25-DEC-2001.
XX	CC	PP 16-APR-2001; 2001WO-US08656.
XX	CC	PR 18-APR-2000; 2000US-055329.
XX	CC	PR 26-JAN-2001; 2001US-0770160.
XX	CC	PA (HYSEQ-) HYSEQ INC.
XX	CC	PT Tang YT, Liu C, Drmanac RT;
XX	CC	DR Tang YT, Liu C, Drmanac RT;
PS	CC	Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
PS	CC	Claim 20; Page 167; 765pp; English.
XX	CC	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of Polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC	immune suppression and/or stimulation; as anti-inflammatory agents; and	Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
CC	in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid										
CC	sequences of novel human secreted proteins of the invention.										
XX											
SQ	Sequence 289 AA;										
	Query Match 100.0%; Score 64; DB 22; Length 289;										
	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;										
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;										
Qy	1 DAHKSEVAHRFK 12	RESULT 25									
ID	AAR14178	AAU29581	Score 64;	DB 12;	Length 303;						
ID	AAR14178 standard; protein; 303 AA.	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
Db	37 DAHKSEVAHRFK 48	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
RESULT 24											
AAU29581	AAU29581 standard; Protein; 289 AA.										
ID	AAU29581;										
AC											
XX											
DT	18-DEC-2001 (first entry)	RESULT 25									
XX		AAU29581;	Score 64;	DB 12;	Length 303;						
DE	Novel human secreted protein #72.	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
DE	Human; vaccination; gene therapy; nutritional supplement;	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;										
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.										
OS	Homo sapiens.										
OS	XX										
PN	XX										
PN	WO200179449-A2.										
PN	25-OCT-2001.										
PD											
PF	16-APR-2001; 2001WO-US086556.	RESULT 25									
XX		AAU29581;	Score 64;	DB 12;	Length 303;						
PR	18-APR-2000; 2000US-0552929.	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
PR	26-JAN-2001; 2001US-0770160.	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
XX											
PA	(HYSE-) HYSEQ INC.										
XX											
PT	Tang YT, Liu C, Drmanac RT;										
PT	XX										
DR	WPI; 2001-611725/70.										
XX											
PT	Nucleic acids encoding a range of human secreted polypeptides, useful in genetic										
PT	vaccination, testing and therapy -										
XX											
CC	The invention relates to novel human secreted polypeptides. The	RESULT 26									
CC	polypeptides and antibodies to the polypeptides are useful for	AAU29581;	Score 64;	DB 12;	Length 303;						
CC	determining the presence of or predisposition to a disease associated	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
CC	with altered levels of polypeptide. The polypeptides are also useful for	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
CC	identifying agents (agonists and antagonists) that bind to them. Cells										
CC	expressing the proteins are useful for identifying a therapeutic agent										
CC	for use in treatment of a pathology related to aberrant expression or										
CC	physiological interactions of the polypeptide. Vectors comprising										
CC	the nucleic acids encoding the polypeptides and cells genetically										
CC	engineered to express them are also useful for producing the proteins.										
CC	The proteins are useful in genetic vaccination, testing and										
CC	therapy, and can be used as nutritional supplements. They may be used to										
CC	increase stem cell proliferation; to regulate haemopoiesis; and in										
CC	bone, cartilage, tendon and/or nerve tissue growth or regeneration;										
CC	immune suppression and/or stimulation; as anti-inflammatory agents; and										
CC	in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid										
CC	sequences of novel human secreted proteins of the invention.										
XX											
SQ	Sequence 289 AA;										
	Query Match 100.0%; Score 64; DB 22; Length 289;										
	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;										
Qy	1 DAHKSEVAHRFK 12	RESULT 25									
ID	AAU29581	AAU29581 standard; Protein; 289 AA.									
Db	37 DAHKSEVAHRFK 48	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
RESULT 24											
AAU29581	AAU29581 standard; Protein; 289 AA.										
ID	AAU29581;										
AC											
XX											
DT	18-DEC-2001 (first entry)	RESULT 25									
XX		AAU29581;	Score 64;	DB 12;	Length 303;						
DE	Novel human secreted protein #72.	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
DE	Human; vaccination; gene therapy; nutritional supplement;	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;										
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.										
OS	Homo sapiens.										
OS	XX										
PN	XX										
PN	WO200179449-A2.										
PN	25-OCT-2001.										
PD											
PF	16-APR-2001; 2001WO-US086556.										
XX											
PR	18-APR-2000; 2000US-0552929.										
PR	26-JAN-2001; 2001US-0770160.										
XX											
PA	(HYSE-) HYSEQ INC.										
XX											
PT	Tang YT, Liu C, Drmanac RT;										
PT	XX										
DR	WPI; 2001-611725/70.										
XX											
PT	Nucleic acids encoding a range of human secreted polypeptides, useful in genetic										
PT	vaccination, testing and therapy -										
XX											
CC	The invention relates to novel human secreted polypeptides. The	RESULT 26									
CC	polypeptides and antibodies to the polypeptides are useful for	AAU29581;	Score 64;	DB 12;	Length 303;						
CC	determining the presence of or predisposition to a disease associated	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
CC	with altered levels of polypeptide. The polypeptides are also useful for	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
CC	identifying agents (agonists and antagonists) that bind to them. Cells										
CC	expressing the proteins are useful for identifying a therapeutic agent										
CC	for use in treatment of a pathology related to aberrant expression or										
CC	physiological interactions of the polypeptide. Vectors comprising										
CC	the nucleic acids encoding the polypeptides and cells genetically										
CC	engineered to express them are also useful for producing the proteins.										
CC	The proteins are useful in genetic vaccination, testing and										
CC	therapy, and can be used as nutritional supplements. They may be used to										
CC	increase stem cell proliferation; to regulate haemopoiesis; and in										
CC	bone, cartilage, tendon and/or nerve tissue growth or regeneration;										
CC	immune suppression and/or stimulation; as anti-inflammatory agents; and										
CC	in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid										
CC	sequences of novel human secreted proteins of the invention.										
XX											
SQ	Sequence 289 AA;										
	Query Match 100.0%; Score 64; DB 22; Length 289;										
	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;										
Qy	1 DAHKSEVAHRFK 12	RESULT 25									
ID	AAU29581	AAU29581 standard; Protein; 289 AA.									
Db	37 DAHKSEVAHRFK 48	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
RESULT 24											
AAU29581	AAU29581 standard; Protein; 289 AA.										
ID	AAU29581;										
AC											
XX											
DT	18-DEC-2001 (first entry)	RESULT 25									
XX		AAU29581;	Score 64;	DB 12;	Length 303;						
DE	Novel human secreted protein #72.	Best Local Similarity 100.0%; Pred. No. 0.0005; Mismatches 0; Indels 0; Gaps 0;									
DE	Human; vaccination; gene therapy; nutritional supplement;	Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;										
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.										
OS	Homo sapiens.										
OS	XX										
PN	XX										
PN	WO200179449-A2.										
PN	25-OCT-2001.										
PD											
PF	16-APR-2001; 2001WO-US086556.										
XX											
PR	18-APR-2000; 2000US-0552929.										
PR	26-JAN-2001; 2001US-0770160.										
XX											
PA	(HYSE-) HYSEQ INC.										
XX											
PT	Tang YT, Liu C, Drmanac RT;										
PT	XX										
DR	WPI; 2001-611725/70.										
XX											
PT	Nucleic acids encoding a range of human secreted polypeptides, useful in genetic										
PT	vaccination, testing and therapy -										
XX											
CC	The invention relates to novel human secreted polypeptides. The	RESULT 26									
CC	polypeptides and antibodies to the polypeptides are useful for	AA									

PF 25-OCT-1988; 88EP-0310000.
 XX
 PR 30-OCT-1987; 87GB-0025529.
 XX
 PA (DELT) DELTA BIOTECH LTD.
 XX
 PT Baillance DJ, Hinchliffe E, Geisow MJ, Senior RJ;
 XX
 DR WPI; 1989-186464/26.
 XX
 PT New N-terminal fragments of human serum albumin
 - esp. useful as blood plasma expanders.
 XX
 PS claim 2; page 9; 20pp; English.
 XX
 CC N-terminal portion of human serum albumin. Used as plasma expanders,
 or as substitutes for HSA or BSA, in tissue culture media.
 XX
 SQ Sequence 373 AA;
 RESULT 27
 AAP90389
 ID AAP90389 standard; protein; 388 AA.
 XX
 AC AAP90389;
 XX
 DT 01-NOV-1989 (first entry)
 DE N-terminal human serum albumin.
 XX
 QY 1 DAHKSEVAHRFK 12
 DB 1 DAHKSEVAHRFK 12
 XX
 PR 28-JUN-1989.
 XX
 PT Best Local Similarity 100.0%; Pred. No. 0.00068; Length 373;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 PA (DELT) DELTA BIOTECH LTD.
 XX
 PI Baillance DJ, Hinchliffe E, Geisow MJ, Senior RJ;
 XX
 PN EP322094-A.
 XX
 DR WPI; 1989-186464/26.
 XX
 PT New N-terminal fragments of human serum albumin
 - esp. useful as blood plasma expanders.
 XX
 PS Claim 2; page 9; 20pp; English.
 XX
 CC N-terminal portion of human serum albumin. Used to make plasma
 expanders, or as substitutes for HSA or BSA, in tissue culture media.
 XX
 SQ Sequence 389 AA;
 RESULT 28
 AAP90391
 ID AAP90391 standard; protein; 389 AA.
 XX
 AC AAP90391;
 XX
 DT 01-NOV-1989 (first entry)
 DE N-terminal human serum albumin.
 XX
 QY 1 DAHKSEVAHRFK 12
 DB 1 DAHKSEVAHRFK 12
 XX
 PR 28-JUN-1989.
 XX
 PA (DELT) DELTA BIOTECH LTD.
 XX
 PT Baillance DJ, Hinchliffe E, Geisow MJ, Senior RJ;
 XX
 DR WPI; 1989-186464/26.
 XX
 PT New N-terminal fragments of human serum albumin
 - esp. useful as blood plasma expanders.
 XX
 PS Claim 2; page 9; 20pp; English.
 XX
 CC N-terminal fragment of human serum albumin used as plasma expander,
 or as substitutes for HSA or BSA, in tissue culture media.
 XX
 SQ Sequence 388 AA;
 RESULT 29
 AAP90391
 ID AAP90391 standard; protein; 390 AA.
 XX
 AC AAP90391;
 XX
 DT 01-NOV-1989 (first entry)
 DE N-terminal human serum albumin.
 XX
 QY 1 DAHKSEVAHRFK 12
 DB 1 DAHKSEVAHRFK 12
 XX
 PR 28-JUN-1989.
 XX
 PT Best Local Similarity 100.0%; Pred. No. 0.00071; Length 389;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 PA 1 DAHKSEVAHRFK 12
 XX
 PR 25-OCT-1988; 88EP-0310000.
 XX
 PS Homo sapiens (Human).
 XX
 CC N-terminal human serum albumin polypeptide; plasma expanders.
 XX
 OS Homo sapiens (Human).
 XX
 PN EP322094-A.
 XX
 PD 28-JUN-1989.
 XX
 QY 25-OCT-1988; 88EP-0310000.
 XX
 PR 30-OCT-1987; 87GB-0025529.
 XX
 PA (DELT) DELTA BIOTECH LTD.
 XX
 PT Baillance DJ, Hinchliffe E, Geisow MJ, Senior RJ;
 XX
 DR WPI; 1989-186464/26.
 XX
 PT New N-terminal fragments of human serum albumin
 - esp. useful as blood plasma expanders.
 XX
 PS Claim 2; page 9; 20pp; English.
 XX
 CC N-terminal portion of human serum albumin; plasma expanders.
 XX
 OS Homo sapiens (Human).
 XX
 PN EP322094-A.
 XX
 PR 28-JUN-1989.
 XX
 PT Best Local Similarity 100.0%; Pred. No. 0.00071; Length 389;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 PA (DELT) DELTA BIOTECH LTD.

XX
PT Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
XX WPI; 1989-186464/26.
DR
XX
CC New N-terminal fragments of human serum albumin
- esp. useful as blood plasma expanders.

XX
PS Claim 2; page 9; 20pp; English.

XX
CC N-terminal portion of human serum albumin. Used to make new
or as substitutes for HSA or BSA, in tissue culture media.

XX
CC Sequence 390 AA;

Query Match 100.0%; Score 64; DB 10; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.00071; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFK 12
Db 1 DAHKSEVAHRFK 12

RESULT 30
AAU29876
ID AAU29876 standard; Protein: 401 AA.

XX
AC AAU29876.
XX
DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #367.
XX Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; Leukaemia.
OS Homo sapiens.
XX
PN WO200173449-A2.

XX
PD 25-OCT-2001.
XX
PP 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US5-0552929.
PR 26-JAN-2001; 2001US-0770160.

(HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Dumanac RT;
XX DR
XX
WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic
vaccination, testing and therapy -

XX PS Claim 20; Page 206; 76pp; English.

The invention relates to novel human secreted polypeptides. The
polypeptides and antibodies to the polypeptides are useful for
determining the presence of or predisposition to a disease associated
with altered levels of polypeptide. The polypeptides are also useful for
identifying agents (agonists and antagonists) that bind to them. Cells
expressing the proteins are useful for identifying a therapeutic agent
for use in treatment of a pathology related to aberrant expression or
physiological interactions of the polypeptide. Vectors comprising
the nucleic acids encoding the polypeptides and cells genetically
engineered to express them are also useful for producing the proteins.
The proteins are useful in genetic vaccination, testing and
therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haemopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU9510-AAU3304 represent the amino acid
sequences of novel human secreted proteins of the invention.

XX
PS Sequence 401 AA;

Query Match 100.0%; Score 64; DB 22; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.00074; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFK 12
Db 38 DAHKSEVAHRFK 49

RESULT 31
AAU29876
ID AAP90392 standard; protein: 407 AA.

XX
AC AAP90392;
XX DT 01-NOV-1989 (first entry)

XX DE N-terminal human serum albumin.
XX KW Human serum albumin; mature protein; new polypeptides;
KW plasma expanders.

XX OS Homo sapiens (Human).

XX PN EP322094-A.

XX PD 28-JUN-1989.

XX PP 25-OCT-1988; 88EP-0310000.

XX PR 30-OCT-1987; 87GB-0025529.

XX PA (DELT) DELTA BIOTCH LTD.

XX PT Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;

XX DR WPI; 1989-186464/26.

XX PT New N-terminal fragments of human serum albumin

PT - esp. useful as blood plasma expanders.

XX PS Claim 2; page 9; 20pp; English.

XX N-terminal portion of human serum albumin. Used to make

CC plasma expanders, or as substitutes for HSA or BSA,
CC in tissue culture media.

XX
SQ Sequence 407 AA;

Query Match 100.0%; Score 64; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.00075; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 1 DAHKSEVAHRFK 12

RESULT 32
AAU29877
ID AAU29877 standard; Protein: 550 AA.

XX
AC AAU29877;
XX DT 18-DEC-2001 (first entry)

XX
 DE Novel human secreted protein #368.
 XX
 PN EP308381-A.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 stem cell proliferation; haemopoiesis; nerve tissue regeneration;
 immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 WO20017949-A2.
 XX
 PD 25-OCT-2001.
 XX
 PR 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2001; 2000US-0552929.
 XX
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 vaccination, testing and therapy -
 XX
 PS Claim 20; Page 206; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haemopoiesis; and in
 CC bone, cartilage, tendon, and/or nerve tissue growth or regeneration; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 Sequence 550 AA;
 QY Query Match 100.0%; Score 64; DB 22; Length 550;
 BET Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0;
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 CC
 QY 1 DAHKSEVAHRPK 12
 DB 1 DAHKSEVAHRPK 12
 SQ Sequence 585 AA;
 QY Query Match 100.0%; Score 64; DB 10; Length 585;
 BET Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0;
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 DB 1 DAHKSEVAHRPK 12
 RESULT 34
 ID AAP90388
 ID AAP90388 standard; protein; 585 AA.
 XX
 AC AAP90388;
 XX
 DT 01-NOV-1989 (first entry)
 XX
 DE Mature human serum albumin polypeptide.
 XX
 KW Human serum albumin; mature protein; new polypeptides;
 KW plasma expanders.
 XX
 OS Homo sapiens (Human).
 XX
 PN EP322094-A.
 XX
 PD 28-JUN-1989.
 XX
 PR 25-OCT-1988; 88EP-0310000.
 XX
 PR 30-OCT-1987; 87GB-0025529.
 XX
 PA (DELT) DELTA BIOTECH LTD.
 XX
 PI Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
 XX
 DR Wei; 1989-186464/26.
 DR N-PSDB; AAN90128.
 XX
 PT New N-terminal fragments of human serum albumin

RESULT 33
 AAP93344
 ID AAP93344 standard; protein; 585 AA.
 XX
 AC AAP93344;
 XX
 DT 23-JUN-1990 (first entry)
 XX
 DE sequence of mature human serum albumin (HSA) as encoded by
 artificial gene.
 XX
 KW Mature human serum albumin; artificial gene; oligonucleotide block;
 XX
 OS Homo sapiens.

PT - esp. useful as blood plasma expanders.

XX

PS Disclosure; fig 2; 20pp; English.

XX

CC Mature protein of human serum albumin (see corresp. AAN90128). Used to make new N-terminal fragments which are used as plasma expanders, or as substitutes for HSA or BSA, in tissue culture media.

CC

XX Sequence 585 AA;

Query Match 100.0%; Score 64; DB 10; Length 585; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12

Db 1 DAHKSEVAHRFK 12

RESULT 35

AAP91422 AAP91422 standard; protein; 585 AA.

ID AAC05318

ID AAC05318 standard; protein; 585 AA.

XX

AC AAC05318;

XX DT 08-OCT-1990 (first entry)

XX DE Human serum albumin gene product.

XX KN Human serum albumin; HSA-A; yeast; ds.

XX OS Homo sapiens.

XX PN JP02117384-A.

XX PD 01-MAY-1990.

XX PF 26-OCT-1988; 88JP-0268302.

XX PR 26-OCT-1988; 88JP-0268302.

XX PA (TOFU) TOA NENRYO KOGYO KK.

XX DR WPI: 1990-176228/23.

XX N-PSDB; AAQ04719.

XX Human serum albumin prepn. by yeast host -

PT by culturing transformed plasmid yeast to produce serum, and

PT removing it.

XX PS Disclosure; ; PP; Japanese.

XX Mature HSA-A may be produced using the sequence incorporated into a

CC plasmid vector with suitable controllers, and transferred to a yeast

CC expression system.

XX Sequence 585 AA;

Query Match 100.0%; Score 64; DB 11; Length 585; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12

Db 1 DAHKSEVAHRFK 12

RESULT 36

AAR05318

ID AAR05318 standard; protein; 585 AA.

XX

AC AAR05318;

XX DT 08-OCT-1990 (first entry)

XX DE Human serum albumin gene product.

XX KN Human serum albumin; HSA-A; yeast; ds.

XX OS Homo sapiens.

XX PN JP02117384-A.

XX PD 01-MAY-1990.

XX PF 26-OCT-1988; 88JP-0268302.

XX PR 26-OCT-1988; 88JP-0268302.

XX PA (TOFU) TOA NENRYO KOGYO KK.

XX DR WPI: 1990-176228/23.

XX N-PSDB; AAQ04719.

XX Human serum albumin prepn. by yeast host -

PT by culturing transformed plasmid yeast to produce serum, and

PT removing it.

XX PS Disclosure; ; PP; Japanese.

XX Mature HSA-A may be produced using the sequence incorporated into a

CC plasmid vector with suitable controllers, and transferred to a yeast

CC expression system.

XX Sequence 585 AA;

Query Match 100.0%; Score 64; DB 11; Length 585; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12

Db 1 DAHKSEVAHRFK 12

RESULT 37

AAR08457

ID AAR08457 standard; Protein; 585 AA.

XX

AC AAR08457;

XX DT 16-APR-1991 (first entry)

XX DE Human serum albumin.

XX HSA; folding; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 123..303 /label=A

FT Region 1..303 /label=B

FT Region /label=C

FT Region /label=B

FT Region /label=C

PN JP02227079-A.

XX PD 25-AUG-1989.

XX
PF 10-SEP-1990; 90JP-0250926.
XX PR 06-OCT-1988; 88JP-0250926.
XX PA (TOPU) TONEN CORP.
XX DR WPI; 1990-317325/42.
XX DR N-PADB; AAQ06099.
PT New human serum albumin fragments - used to bond medicines and for
PT stable folding of protein(s).
XX SQ Sequence 585 AA;
PS Claim 1; Fig 8; 24pp; Japanese.
XX
CC Fragments A-C of HSA are expressed as fusion proteins with the
CC signal peptide of E. coli alkaline phosphatase. The fragments are
selected for their specific properties. The C-terminal truncated
fragment, B, does not bind long-chain fatty acids but does bind to
various medicines at the central region. The N-terminal truncated
fragment, C, has good stability in protein folding. The central
CC segment, A, has characteristics of both B and C.
CC See also AAQ06096-Q06098.

XX Sequence 585 AA;
SQ Sequence 585 AA;
XX Query Match 100.0%; Score 64; DB 11; Length 585;
XX Best Local Similarity 100.0%; Pred. No. 0.0011; Pred. No. 0.0011;
XX Matches 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRPK 12
Db 1 DAHKSEVAHRPK 12

RESULT 39
AAR26207
ID AAR26207 standard; Protein; 585 AA.
XX AC AAR26207;
XX DT 08-FEB-1993 (first entry)
XX DE Human serum albumin.
XX KW Expression cassette; methanol-responsive gene; methylotrophic yeast;
KW alpha-mating factor; AMF; HSA.
XX OS Homo sapiens.
XX PN WO9213951-A.
XX PD 20-AUG-1992.
XX PF 04-FEB-1992; 92W0-US01015.
XX PR 04-FEB-1991; 91US-0650040.
XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX PI Davis GR, PROVOST SA;
XX DR WPI; 1992-300037/36.
XX N-PADB; AAQ2462.
XX PT DNA fragment for prodn. of human serum albumin - comprises
PT expression cassette including promoter and terminator sequences
PT of methanol responsive gene, for expression in methylo trophic
PT yeast.
XX PS Disclosure; Page 50-1; 75pp; English.
XX CC The sequences given in AAR26207-9 were encoded by an expression cassette
CC containing:
CC (a) the promoter region of a methanol-responsive gene of
CC a methylo trophic Yeast;
CC (b) a DNA sequence encoding a polypeptide encoding
CC (i) a secretion signal from either *S. cerevisiae* alpha-
CC mating factor (AMF) pre-pro sequence (AAR26208) or the native human
CC serum albumin (HSA) signal sequence; and
CC (ii) an HSA peptide (AAR26207); and
CC (c) a transcription terminator, functional in methylo trophic
CC yeast (AAR26209).
CC The expression vector encoding this protein can be used for the large
CC scale production of HSA. The HSA can then be administered to patients
CC with circulatory failure or albumin depletion.
XX SQ Sequence 585 AA;
XX Query Match 100.0%; Score 64; DB 13; Length 585;
XX Best Local Similarity 100.0%; Pred. No. 0.0011; Pred. No. 0.0011;
XX Matches 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRPK 12
Db 1 DAHKSEVAHRPK 12

XX HSA can be recombinantly produced in yeast. A HSA coding
CC sequence is incorporated into a vector which also contains a DNA
CC region having the same base sequence as that of the target region
CC of the chromosome and a promoter (e.g., HIS4 or LEU2) to regulate
PT the expression of the HSA coding sequence in the yeast host.
XX etc. is inserted
PS Disclosure; Fig 4; 12pp; Japanese.

Query Match 100.0%; Score 64; DB 18; length 585;
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12

RESULT 43
 AAW59841
 ID AAW59841 standard; Protein: 585 AA.
 AC AAW59841;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Mature protein of human serum albumin (HSA).
 XY
 Protein expression; monocotyledon plant cell;
 glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III;
 ATIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema;
 KW antithrombotic; blood replacement.
 XX
 OS Homo sapiens.
 XX
 PN WO9836085-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 99WO-US03068.
 XX
 PR 13-FEB-1997; 97US-0038170.
 PR 13-FEB-1997; 97US-0037991.
 PR 13-FEB-1997; 97US-0038168.
 PR 13-FEB-1997; 97US-0038169.
 XX
 (PHYT-) APPLIED PHYTOLOGICS INC.
 XX
 PT Rodriguez RL, Sutliff TD;
 XX
 DR WPI; 1998-467179/40.
 XX
 PT Expressing mature, glycosylated proteins in monocotyledonous plant
 cells - from chimeric gene including signal peptide sequence,
 specifically therapeutic agents and industrial enzymes
 PT Disclosure; Pages 31-32; 52pp; English.

XX
 CC The present sequence represents the mature protein of human serum
 albumin (HSA). The protein is used to exemplify the invention. The
 specification describes a method for producing mature heterologous
 protein in monocotyledonous plant cells. The method comprises
 transforming the cells with a chimeric gene comprising a monocotyledon
 transcription regulator, inducible either during seed maturation or by
 adding/removing a small molecule, DNA encoding the heterologous protein,
 and DNA encoding a signal peptide causing
 secretion of the protein from the cell. Proteins expressed in this
 manner include mature glycosylated alpha 1-antitrypsin (AAT) with a
 glycosylation pattern that significantly increases its serum half-life.
 mature glycosylated antithrombin III (ATIII), mature human serum albumin
 (HSA) having the native folding pattern as shown by bilirubin-binding
 characteristics, or mature active subtilisin BPN'. These proteins are
 useful therapeutically (e.g. AAT for treating emphysema, ATIII as
 antithrombotic and HSA as blood replacement) or as industrial enzymes
 (BPN' is used in detergents).

SQ Sequence 585 AA;

Query Match 100.0%; Score 64; DB 19; Length 585;
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12

RESULT 44
 AAY84873
 ID AAY84873 standard; protein; 585 AA.
 AC AAY84873;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Amino acid sequence of a human albumin protein.
 XX
 Human; albumin; ischemic state; serum protein; metal ion salt;
 KW perioperative ischemia; ischemia; myocardial infarction;
 KW progressive coronary artery disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Modified-site Location/Qualifiers
 FT /note= "optionally acetylated, and claimed under
 FT claim 56"
 XX
 PN WO20020840-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US22905.
 XX
 PR 02-OCT-1998; 98US-0102738.
 PR 02-OCT-1998; 98US-0165581.
 PR 02-OCT-1998; 98US-0165926.
 PR 11-JAN-1999; 99US-0115392.
 XX
 PA (ISCH-) ISCHEMIA TECHNOLOGIES INC.
 XX
 PT Bar-Or D, Lau E, Winkler JV;
 XX
 DR WPI; 2000-303843/26.
 XX
 PT New method for the continuous detection of ischemic states comprises
 PT detecting and quantifying the existence of an alteration of the serum
 PT protein albumin -
 XX
 PS Disclosure; Page 97-100; 105pp; English.
 XX
 CC The present sequence represents human albumin protein. The specification
 CC describes a method for the continuous detection of ischemic states. The
 CC method comprises detecting and quantifying the existence of an alteration
 CC of the serum protein albumin. The method comprises contacting a
 CC biological sample containing albumin from the patient with an excess
 CC quantity of a metal ion salt, where the metal ion binds to the N-terminus
 CC of naturally occurring human albumin, to form a mixture containing bound
 CC metal ions and unbound metal ions, and then determining the amount of
 CC metal ions bound to the albumin N-terminus. The amount of bound metal
 CC ions is correlated to a known value to determine the occurrence or
 CC non-occurrence of an ischemic event. The methods are useful for detection
 CC of ischemic states. The methods are also useful for distinguishing
 CC perioperative ischemia from ischemia caused by, amongst other things,
 CC myocardial infarctions and progressive coronary artery disease.
 XX
 SQ Sequence 585 AA;

Query Match 100.0%; Score 64; DB 21; Length 585;
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12

Db 1 DAHKSEVAHRFK 12
 RESULT 45
 AAY83946 standard; Protein; 585 AA.
 XX
 AC AAY83946;
 XX
 DR 28-JUL-2000 (first entry)
 XX
 DE Yeast codon-biased recombinant human serum albumin protein.
 KW Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
 KW overlapping oligonucleotide; expression vector.
 XX
 OS Homo sapiens.
 XX
 Synthetic.
 XX
 CN1239103-A.
 XX
 DO 22-DEC-1999.
 XX
 PR 17-JUN-1998; 98CN-0102506.
 XX
 PA (HAIJ-) HALTI BIOENGINEERING CO LTD.
 XX
 PT Li S, Lu D;
 XX
 DR WPI; 2000-351198/31.
 XX
 N-PSDB; AAA10091.
 PT Process for preparing recombinant human serum albumin - which comprises
 PT yeast biased sex codons
 XX
 PS Disclosure; Fig 1; 44pp; Chinese.
 XX
 CC The method relates to a method of recombinantly producing human serum
 albumin (HSA) in yeast by altering the coding sequence of HSA to
 comprise a yeast codon bias. The complete HSA gene (AAA10091) was
 generated as three synthetic fragments (AAA10092-A10094) joined by
 recombinant DNA technology. Each HSA fragment was synthesised from
 overlapping oligonucleotide fragments that were extended. This sequence
 represents the complete sequence of the HSA encoded by the human gene
 with a yeast codon bias. The invention also covers a recombinant
 expression vector, yeast host cells carrying the recombinant expression
 vector and the process for producing human serum albumin in the yeast
 host cell, especially in secretory mode.
 XX
 SQ Sequence 585 AA:
 Query Match 100.0%; Score 64; DB 21; Length 585;
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0;
 Matches 12; Conservative 0; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12
 RESULT 46
 ABB79006
 ID ABB79006 standard; Protein; 585 AA.
 XX
 AC ABB79006;
 XX
 DT 01-AUG-2002 (first entry)
 XX
 DE Human mature albumin protein SEQ ID NO:18.
 KW Human; growth hormone; hGH; albumin; human serum albumin; HSA;

KW albumin fusion protein; cytostatic; anorectic; immunosuppressive;
 KW antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer;
 KW non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis;
 KW type I diabetes mellitus; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..194
 FT /Label= 1
 FT Domain 1..105
 FT /Label= subdomain
 FT Disulfide-bond 53..62
 FT Disulfide-bond 75..91
 FT Disulfide-bond 90..101
 FT Region 106..119
 FT /note= "flexible inter-subdomain linker region"
 FT Domain 120..194
 FT /Label= subdomain
 FT Disulfide-bond 124..169
 FT Disulfide-bond 168..177
 FT Domain 195..387
 FT /Label= 2
 FT Domain 195..291
 FT Disulfide-bond 245..253
 FT Disulfide-bond 265..279
 FT Disulfide-bond 278..289
 FT Region 292..315
 FT Domain /note= "flexible inter-subdomain linker region"
 FT /Label= subdomain
 FT Disulfide-bond 316..387
 FT Disulfide-bond 316..361
 FT Disulfide-bond 360..369
 FT Domain 388..585
 FT /Label= 3
 FT Domain 388..491
 FT /Label= subdomain
 FT Disulfide-bond 392..438
 FT Disulfide-bond 437..448
 FT Disulfide-bond 461..477
 FT Disulfide-bond 476..487
 FT Region 492..511
 FT /note= "flexible inter-subdomain linker region"
 FT Domain 512..585
 FT /Label= subdomain
 FT Disulfide-bond 514..559
 FT Disulfide-bond 558..567
 XX WO200179442-A2.
 PN WO200179442-A2.
 XX
 PD 25-OCT-2001.
 XX
 PR 12-APR-2001; 2001WO-US11850.
 XX
 PR 12-APR-2000; 2000US-229358P.
 PR 25-APR-2000; 2000US-193845P.
 PR 21-DEC-2000; 2000US-256931P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Haseltine WA;
 XX
 DR WPI; 2001-611723/70.
 XX
 N-PSDB; ABN07288.
 XX
 PT New albumin fusion proteins, useful for treating diseases and disorders
 PT such as cancer, comprise therapeutic protein fused to albumin -
 XX
 PS Claim 1; Fig 11; 413pp; English.
 XX
 CC The present invention describes an albumin fusion protein (1) comprising
 a therapeutic protein: X and (a fragment or variant of) albumin

KW glomerulonephritis; cardiovascular disorder; arrhythmia; rhinitis;
 KW respiratory disorder; neurologic disease; Alzheimer's disease;
 KW endocrine disorder; phaeochromocytoma; reproductive system disorder;
 KW measles; gastrointestinal disorder; irritable bowel syndrome; HIV;
 KW human immunodeficiency virus; wound healing; renal cell carcinoma;
 KW melanoma; gene therapy.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Domain 54..61 /label= Loop_I

FT Domain 76..89 /label= Loop_II

FT Domain 92..100 /label= Loop_III

FT Domain 170..176 /label= Loop_IV

FT Domain 247..252 /label= Loop_V

FT Domain 266..277 /label= Loop_VI

FT Domain 280..288 /label= Loop_VII

FT Domain 362..368 /label= Loop_VIII

FT Domain 439..447 /label= Loop_IX

FT Domain 461..475 /label= Loop_X

FT Domain 478..486 /label= Loop_XI

FT Domain 560..566 /label= Loop_XII

PN WO200179258-A1.

XX PD 25-OCT-2001.

XX PF 12-APR-2001; 2001WO-US12008.

XX PR 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (PRIN-) PRINCIPIA PHARM CORP.

XX Rosen CA, Sadeghi H, Prior CP, Turner AJ;

DR WPI; 2001-602931/68.

XX N-PSDB; AAD22287.

PT Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human immunodeficiency virus) or infection -

PS Claim 1; Fig 9; 325pp; English.

XX The invention relates to albumin fusion proteins comprising therapeutic protein and human albumin (HA). The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (transplant rejection); blood related disorders (myocardial infarction); hyperproliferative disorders (childhood acute myeloid leukaemia); renal disorder (glomerulonephritis); cardiovascular disorders (arrhythmias); respiratory disorders (e.g. non-allergic rhinitis); endocrine disorders (phaeochromocytoma); reproductive system disorders (syphilis); infectious diseases (measles); gastrointestinal disorders (irritable bowel syndrome) and wound healing. The albumin fusion proteins are also used in the treatment of metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma and HIV (human

CC immunodeficiency virus) infection. Nucleic acid encoding albumin fusion protein is useful in gene therapy. The present sequence is human protein (HA) protein.

CC albumin (HA) protein.

XX Sequence 585 AA;

Query Match 100.0%; Score 64; DB 22; Length 585; Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0; Matches 12; Conservative 0; Sequence 585 AA;

Db 1 DAHKSEVAHRFK 12

RESULT 49

ID AAMS2567

ID AAMS2567 standard; Protein; 585 AA.

XX AC AAMS2567;

XX DT 05-FEB-2002 (first entry)

XX DE Mature human serum albumin.

XX Human; serum albumin; HA; antiinflammatory; immunosuppressive; cardiotonic; nootropic; neuroprotective; gene therapy; immune disorder; wound healing; hyperproliferative disorder; renal disorder; cardiovascular disorder; respiratory disorder; neurological disease; endocrine disorder; reproductive system disorder; infectious disease; gastrointestinal disorder.

XX KW Homo sapiens.

XX OS Homo sapiens.

PN WO200179444-A2.

XX PD 25-OCT-2001.

XX PF 12-APR-2001; 2001WO-US12013.

XX PR 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (PRIN-) PRINCIPIA PHARM CORP.

XX Rosen CA, Haseltine WA;

DR WPI; 2001-616755/71.

XX N-PSDB; ABA03057.

PT Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders -

XX Claim 1; Fig 15; 606pp; English.

The present invention relates to albumin fusion proteins, which comprise a therapeutic protein and albumin. The present sequence is the protein sequence for mature human serum albumin (HA), which was used to generate the fusion proteins of the present invention. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (arrhythmias), non-allergic rhinitis, endocrine disorders (phaeochromocytoma), reproductive system disorders (syphilis), infectious diseases (measles), gastrointestinal disorders (irritable bowel syndrome) and wound healing. The albumin fusion proteins are also used in the treatment of metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma and HIV (human

SQ Sequence 585 AA;

Query Match 100.0%; Score 64; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHFK 12
 |||||
 Db 1 DAHKSEVAHFK 12

RESULT 50

AAE13129
 ID AAE13129 standard; Protein; 585 AA.

XX AAE13129;

AC

XX DT 28-JAN-2002 (first entry)

XY Human albumin (HA).

KW Human; albumin; HA; fusion protein; therapeutic protein; vulnerability; immune system disorder; transplant rejection; blood related disorder; myocardial infarction; hyperproliferative disorder; glomerulonephritis; childhood acute myeloid leukaemia; cardiovascular disorder; arrhythmia; respiratory disorder; gene therapy; non-allergic rhinitis; notropic; neurological disease; Alzheimer's disease; reproductive system disorder; endocrine disorder; pheochromocytoma; infectious disease; antiarthritic; measles; gastrointestinal disorder; irritable bowel syndrome; Syphilis; wound healing; antiinflammatory; immunosuppressive; neoprotective; cardiotonic; cytostatic; antileukaemic; antirheumatic; antimicrobial; renal disorder.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT Domain 54..61 /label= Loop_I

FT Domain 76..89 /label= Loop_II

FT Domain 92..100 /label= Loop_III

FT Domain 170..176 /label= Loop_IV

FT Domain 247..252 /label= Loop_V

FT Domain 266..277 /label= Loop_VI

FT Domain 280..288 /label= Loop_VII

FT Domain 362..368 /label= Loop_VIII

FT Domain 439..447 /label= Loop_VX

FT Domain 461..475 /label= Loop_X

FT Domain 478..486 /label= Loop_XI

FT Domain 560..566 /label= Loop_XII

PN WO200179443-A2.

XX

PD 25-OCT-2001.

XX

PF 12-APR-2001; 2001WO-US11924.

XX

PR 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-193384P.

PR 21-DEC-2000; 2000US-256931P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Haseltine WA;

XX WPI; 2001-616754/71.

DR N-PSDB; ADD21638.

XX PT Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders -

XX PS Claim 1; Fig 9; 30pp; English.

CC The invention relates to albumin fusion proteins comprising therapeutic protein and human albumin (HA). Therapeutic protein fused to albumin have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia), renal disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome) and wound healing. Nucleic acids encoding albumin fusion protein is used in gene therapy. The present sequence is human albumin (HA) protein.

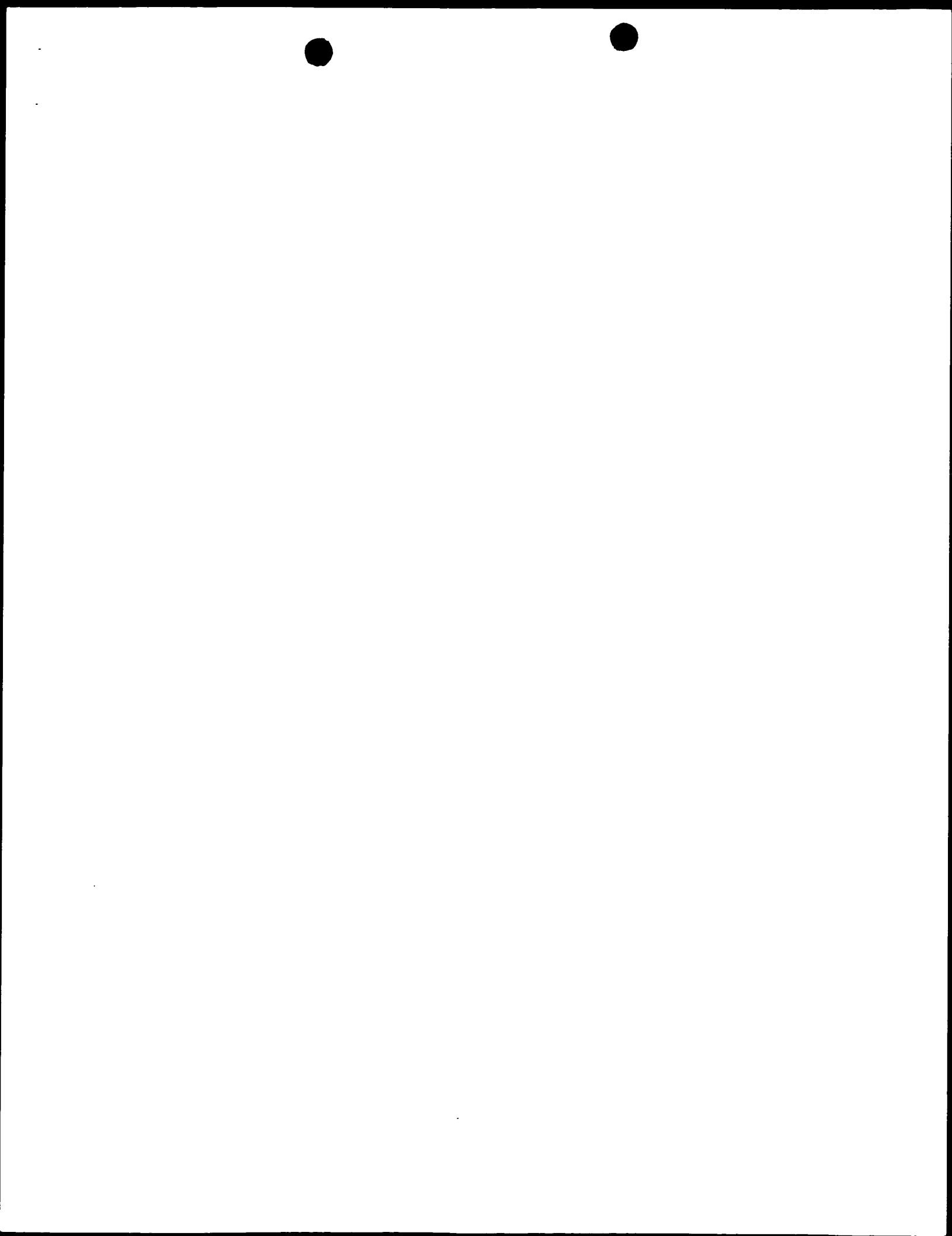
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 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHFK 12
 |||||
 Db 1 DAHKSEVAHFK 12

Search completed: April 11, 2003, 15:18:31.
 Job time : 39 secs



GenCore version 5.1.4.p5 4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Title: US-09-846-347-1

Perfect score:

64

Sequence:

1 DAHKSEVAHRFK 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Post-processing: Minimum Match 0%

Maximum DB seq length: 0

Minimum DB seq length: 200000000

Number of hits satisfying chosen parameters: 262574

Listed first 75 summaries

Database : ISSUED PATENTS AA:
 1: /cgn2_6/pctdata/1/iaa/5A_COMBO.pep.*
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 6: /cgn2_6/pctdata/1/iaa/backfiles1.pep.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	64	100.0	585 1 US-08-153 799-14	Sequence 14, Appli
2	64	100.0	585 1 US-08-448-196A-3	Sequence 3, Appli
3	64	100.0	585 2 US-08-984-176-1	Sequence 1, Appli
4	64	100.0	585 2 US-08-702-572-2	Sequence 2, Appli
5	64	100.0	585 4 US-08-769-746-2	Sequence 2, Appli
6	64	100.0	609 1 US-08-222-619-3	Sequence 3, Appli
7	64	100.0	609 1 US-08-433-037-4	Sequence 4, Appli
8	64	100.0	609 4 US-08-897-956A-2	Sequence 2, Appli
9	64	100.0	609 5 PCT-US95-04075-3	Sequence 3, Appli
10	64	100.0	610 2 US-08-699-2	Sequence 2, Appli
11	64	100.0	783 1 US-08-256-938-2	Sequence 2, Appli
12	64	100.0	787 1 US-08-256-938-4	Sequence 4, Appli
13	64	100.0	787 2 US-08-797-689-15	Sequence 16, Appli
14	64	100.0	978 4 US-08-897-956A-3	Sequence 4, Appli
15	59	92.2	582 1 US-08-134-638-1	Sequence 3, Appli
16	59	92.2	583 1 US-08-448-196A-4	Sequence 2, Appli
17	59	92.2	584 1 US-08-448-196A-7	Sequence 7, Appli
18	58	90.6	13 2 US-08-803-364-7	Sequence 16, Appli
19	58	90.6	13 2 US-08-024-198-13	Sequence 13, Appli
20	58	90.6	13 2 US-09-186-4109-13	Sequence 5, Appli
21	54	84.4	583 1 US-08-448-196A-5	Sequence 6, Appli
22	54	84.4	583 1 US-08-448-196A-6	Sequence 6, Appli
23	50	78.1	13 2 US-08-803-364-6	Sequence 12, Appli
24	50	78.1	13 2 US-09-024-198-12	Sequence 12, Appli
25	50	78.1	13 2 US-09-186-4109-12	Sequence 1, Appli
26	50	78.1	16 2 US-08-803-364-1	Sequence 10, Appli
27	50	78.1	US-09-024-198-10	Sequence 10, Appli

RESULT 1
 US-08-153-799-14
 Sequence 14, Application US/08153799
 Patent No. 576683
 GENERAL INFORMATION:
 APPLICANT: Ballance, David J
 ATTORNEY: Goodey, Andrew R
 TITLE OF INVENTION: Polypeptides
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: R Hain Swope, BOC Health Care Inc
 STREET: 100 Mountain Avenue
 CITY: Murray Hill
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07974
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,799
 FILING DATE: 06-MAR-1992
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 8909916.2
 FILING DATE: 29-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB90/00650
 FILING DATE: 26-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/775952
 FILING DATE: 29-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: SWOPE, R Hain
 REGISTRATION NUMBER: 24864
 REFERENCE/DOCKET NUMBER: 92H032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 655 2400
 TELEFAX: (908) 771 6159
 TELEX: 219484
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Region
 LOCATION: 369..419
 OTHER INFORMATION: /note="Alternative C-termini of
 OTHER INFORMATION: HSA(1-n)"
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..585
 OTHER INFORMATION: /note="Amino acid sequence of
 OTHER INFORMATION: natural HSA"
 US-08-153-799-14

RESULT 2
 US-08-448-196A-3
 Sequence 3, Application US/08448196A
 Patent No. 5180594
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C
 APPLICANT: HO, JOSEPH X
 APPLICANT: RUKER, FLORIAN
 TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
 TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER
 FILE REFERENCE: 08/984,176
 CURRENT APPLICATION NUMBER: US/08/984,176
 CURRENT FILING DATE: 1997-12-03
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 585
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-984-176-1

Query Match 100.0%; Score 64; DB 1; length 585;
 Best Local Similarity 100.0%; Pred. No. 0.00049; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mis 0; InDel 0; Gap 0;

Q 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12

RESULT 3
 US-08-984-176-1
 Sequence 1, Application US/08984176
 Patent No. 5948009
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C
 APPLICANT: HO, JOSEPH X
 APPLICANT: RUKER, FLORIAN
 TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
 TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER
 FILE REFERENCE: 08/984,176
 CURRENT APPLICATION NUMBER: US/08/984,176
 CURRENT FILING DATE: 1997-12-03
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 585
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-984-176-1

Query Match 100.0%; Score 64; DB 2; length 585;
 Best Local Similarity 100.0%; Pred. No. 0.00049; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mis 0; InDel 0; Gap 0;

Q 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12

RESULT 4
 US-08-702-572-2
 Sequence 2, Application US/08702572
 Patent No. 595386
 GENERAL INFORMATION:
 APPLICANT: KERRY-WILLIAMS, SEAN M
 APPLICANT: Gilbert, Sarah C
 TITLE OF INVENTION: Yeast Strains and Modified Albumins

ADRESSEE: NASA
 STREET: MARSHALL SPACE FLIGHT CENTER
 CITY: HUNTSVILLE
 STATE: ALABAMA
 COUNTRY: USA
 ZIP: 35812

COMPUTER READABLE FORM:

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Centeon L.L.C.
 STREET: 1020 First Avenue
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406-1310

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,572
 FILING DATE: 11-Nov-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 95/23857
 FILING DATE: 1-MAR-1995
 APPLICATION NUMBER: GB 9404270.2

FILING DATE: 5-MAR-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Naomi Biswas
 REGISTRATION NUMBER: 38,384
 REFERENCE/DOCKET NUMBER: CEO114 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610/878/4294
 TELEFAX: 610/878/4221

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-702-572-2

RESULT 5
 Sequence Match 100.0%; Score 64; DB 2; Length 585;
 Best Local Similarity 100.0%; Pred. No. 0.00049; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0;

Qy 1 DAHKSEVAHRFK 12
 Db 1 DAHKSEVAHRFK 12

RESULT 6
 US-08-222-619-3
 Sequence 3, Application US/08222619
 Patent No. 5652352
 GENERAL INFORMATION:
 APPLICANT: Lichenstein, Henri
 APPLICANT: Lyons, David
 APPLICANT: Wurff, Mark
 APPLICANT: Wright, Samuel
 TITLE OF INVENTION: Afamin, A Human Serum Albumin-Like
 TITLE OF INVENTION: Protein
 NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Center, Patent Operations/RRC
 STREET: 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: U.S.
 ZIP: 91320-1789

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/222,619
 FILING DATE:
 CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 609 amino acids
 TYPE: amino acid
 STRANDBIDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

US-08-222-619-3

Query Match 100.0%; Score 64; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.00051; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0;

Qy 1 DAHKSEVAHRFK 12
 Db 25 DAHKSEVAHRFK 36

RESULT 7
 US-08-433-037-4
 ; Sequence 4, Application US/08433037
 ; Patent No. 5707928
 ; GENERAL INFORMATION:

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/769,746
 FILING DATE: 19-DEC-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Carroll, Peter G.

APPLICANT: Sreekrishna, Kotikanyadan
 APPLICANT: Barr, Kathryn A.
 APPLICANT: Brielle, Russell A.
 APPLICANT: Thill, Gregory P.
 APPLICANT: Tschoop, Juerg F.
 TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
 Tissue
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Scully, Scott, Murphy & Preaser
 STREET: 400 Garden City Plaza
 STATE: New York
 CITY: Garden City
 COUNTRY: U.S.A.
 ZIP: 11530-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/433,037
 FILING DATE: 03-MAY-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: DiGilio, Frank S.
 REFERENCE NUMBER: 31,346
 READING/DOCKET NUMBER: 9108Z
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 609 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-433-037-4

Query Match 100.0%; Score 64; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

ULT 8

US-08-897-956A-2

Sequence 2, Application US/08897956A
 Patent No. 6423512

GENERAL INFORMATION:

APPLICANT: Mary Ellen Digan
 APPLICANT: Philip Lake
 APPLICANT: Hermann Gram
 TITLE OF INVENTION: Fusion Polypeptides
 FILE REFERENCE: 600-724/CPA
 CURRENT APPLICATION NUMBER: US/08/897,956A
 CURRENT FILING DATE: 1997-07-21
 PRIORITY APPLICATION NUMBER: 60/022,689
 PRIOR FILING DATE: 1996-07-26
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 609
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-08-897-956A-2

Query Match 100.0%; Score 64; DB 4; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.00051; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

PCT-US95-04075-3

Sequence 3, Application PC/TUS9504075

GENERAL INFORMATION:

APPLICANT: AMGEN INC
 TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like Protein
 NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSE: Amgen Center, Patent Operations/RRC
 STREET: 1840 Defendalland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: U.S.
 ZIP: 91320-1789

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04075
 FILING DATE:

CLASSIFICATION:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 609 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US95-04075-3

Query Match 100.0%; Score 64; DB 5; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.00051; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

RESULT 10

US-08-797-689-2

Sequence 2, Application US/08797689

PATENT NO. 5876959

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard
 APPLICANT: Fournier, Alain
 APPLICANT: Guittot, Jean-Dominique
 APPLICANT: Jung, Gerard
 APPLICANT: Ven, Patrice
 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
 NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
 ADDRESSE: Rhone Poulen Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh

Query Match 100.0%; Score 64; DB 4; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.00051; Mismatches 0; Indels 0; Gaps 0;

OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3829
 FAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 NAME: Smith Ph.D., Julie K.
 LENGTH: 610 amino acids
 TOPOLogy: linear
 TYPE: amino acid
 MOLECULE TYPE: protein
 US-08-797-689-2

Query Match 100.0%; Score 64; DB 2; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00057; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHRPK 12
 Db 25 DAHKSEVAHRPK 36

RESULT 11
 US-08-256-938-2
 Sequence 2, Application US/08256938
 Patient No. 566583
 GENERAL INFORMATION:
 APPLICANT: Yeh, Patrice
 TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.0 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/256,938
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: FR 92/01065
 FILING DATE: 31-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Goodman, Rosanne
 REGISTRATION NUMBER: 32,534
 REFERENCE/DOCKET NUMBER: ST92007-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3817
 FAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 787 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-256-938-4

Query Match 100.0%; Score 64; DB 1; Length 787;
 Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHRPK 12
 Db 203 DAHKSEVAHRPK 214

RESULT 13
 US-08-797-689-16

Sequence 16, Application US/08797689
 Patent No. 5876969
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 APPLICANT: Fournier, Alain
 APPLICANT: Guilton, Jean-Dominique
 APPLICANT: Jung, Gerard
 APPLICANT: Yeh, Parrice
 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, J343
 CITY: Collegeville
 STATE: PA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 CLASSIFICATION: 435
 PRIORITY DATA:
 PRIORITY NUMBER: US 08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph.D., Julie K.
 REGISTRATION NUMBER: P-38-619
 REFERENCE/DOCKET NUMBER: SP92006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 FAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 787 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 8-797-689-16

Query Match 100.0%; Score 64; DB 2; Length 787;
 Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Strandness 0;

QY 1 DAHKSEVAHRFK 12
 Db 203 DAHKSEVAHRFK 214

RESULT 14
 US-08-897-956A-3
 ; Sequence 3, Application US/08897956A
 ; Patent No. 623512
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Ellen Digan
 ; APPLICANT: Philip Lake
 ; APPLICANT: Hermann Gruner
 ; TITLE OF INVENTION: Fusion Polypeptides
 ; FILE REFERENCE: 600-724/cpa
 ; CURRENT APPLICATION NUMBER: US/08/897,956A
 ; CURRENT FILING DATE: 1997-07-21
 ; PRIORITY APPLICATION NUMBER: 60/022,689

PRIOR FILING DATE: 1996-07-26
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 978
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fusion polypeptide
 US-08-897-956A-3

Query Match 100.0%; Score 64; DB 4; Length 978;
 Best Local Similarity 100.0%; Pred. No. 0.00085; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Strandness 0;

QY 1 DAHKSEVAHRFK 12
 Db 212 DAHKSEVAHRFK 223

RESULT 15
 US-08-134-638-1
 ; Sequence 1, Application US/08134638
 ; Patent No. 5473050
 ; GENERAL INFORMATION:
 ; APPLICANT: Strand, Frederick T
 ; TITLE OF INVENTION: Denatured Bovine Serum Albumin Milk
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Frederick T. Strand
 ; STREET: P.O. Box 64321
 ; CITY: Phoenix
 ; STATE: Arizona
 ; COUNTRY: USA
 ; ZIP: 85082-4321
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb storage
 COMPUTER: IBM PC
 OPERATING SYSTEM: MS-DOS 5.0
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/134,638
 FILING DATE: 10/12/93
 CLASSIFICATION: 530
 PRIORITY DATA:
 PRIORITY NUMBER: N/A
 FILING DATE: N/A
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiss, Harry M
 REGISTRATION NUMBER: 19,497
 REFERENCE/DOCKET NUMBER: 1-95P1423
 TELEPHONE: (602) 947-2663
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 582
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-134-638-1

Query Match 92.2%; Score 59; DB 1; Length 582;
 Best Local Similarity 83.3%; Pred. No. 0.004; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Strandness 1;

QY 1 DAHKSEVAHRFK 12
 Db 1 DTHKSEIAHRFK 12

RESULT 16

US-08-448-196A-4

Sequence 4, Application US/08448196A

PATENT NO. 570594

GENERAL INFORMATION:

APPLICANT: CARTER, DANIEL C.

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS

CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR

TITLE OF INVENTION: RELATED PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NASA

STREET: MARSHALL SPACE FLIGHT CENTER

CITY: HUNTSVILLE

STATE: ALABAMA

COUNTRY: USA

ZIP: 35812

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

ATTORNEY/AGENT INFORMATION:

NAME: BROAD JR., ROBERT L.

REGISTRATION NUMBER: 18,757

REFERENCE/DOCKET NUMBER: XX/MFS-28402-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 205-544-0021

TELEFAX: 205-544-0258

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 583 amino acids

ATTORNEY/AGENT INFORMATION:

NAME: BROAD JR., ROBERT L.

REGISTRATION NUMBER: 16,757

REFERENCE/DOCKET NUMBER: XX/MFS-28402-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 205-544-0021

TELEFAX: 205-544-0258

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 583 amino acids

ATTORNEY/AGENT INFORMATION:

NAME: amino acid

TYPE: linear

TOPOLogy: protein

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

APPLICATION NUMBER: US/08/448,196A

FILING DATE: 23-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: BROAD JR., ROBERT L.

REGISTRATION NUMBER: 16,757

REFERENCE/DOCKET NUMBER: XX/MFS-28402-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 205-544-0021

TELEFAX: 205-544-0258

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 583 amino acids

ATTORNEY/AGENT INFORMATION:

NAME: amino acid

TYPE: linear

TOPOLogy: protein

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

APPLICATION NUMBER: US/08-448-196A-4

FILING DATE: 23-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: amino acid

TYPE: linear

TOPOLogy: protein

MOLECULE TYPE: peptide

RESULT 18

US/08-803-364-7

Sequence 7, Application US/08803364

; Patent No. 5864014

GENERAL INFORMATION:

APPLICANT: PASANO, Alessio

TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEANS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: A-6888

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

ATTORNEY/AGENT INFORMATION:

NAME: amino acid

TYPE: linear

TOPOLogy: protein

MOLECULE TYPE: peptide

RESULT 17

US/08-448-196A-7

Sequence 7, Application US/08448196A

PATENT NO. 570594

GENERAL INFORMATION:

APPLICANT: CARTER, DANIEL C.

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS

CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR

TITLE OF INVENTION: RELATED PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NASA

STREET: MARSHALL SPACE FLIGHT CENTER

CITY: HUNTSVILLE

STATE: ALABAMA

COUNTRY: USA

ZIP: 35812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: A-6888

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

ATTORNEY/AGENT INFORMATION:

NAME: amino acid

TYPE: linear

TOPOLogy: protein

MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; US-09-803-364-7

Query Match 90.6%; Score 58; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 2 AHKSEVAHRFK 12
Db 1 AHKSEVAHRFK 11

RESULT 19

US-09-024-198-13

; Sequence 13, Application US/09024198
; Patent No. 5912323

; GENERAL INFORMATION:

; APPLICANT: FASANO, Alessio

; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

; CITY: Washington, D.C.

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/186,409

; FILING DATE: 5 NOV 1998

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/003,364

; FILING DATE: 20 FEB 1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: KIT, Gordon

; REGISTRATION NUMBER: 30,764

; REFERENCE/DOCKET NUMBER: A-7306

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 293-7060

; FAX: (202) 293-7860

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; HYPOTHETICAL: NO

; US-09-186-409-13

Query Match 90.6%; Score 58; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 2 AHKSEVAHRFK 12
Db 1 AHKSEVAHRFK 11

RESULT 21

US-08-48-196A-5

; Sequence 5, Application US/08448196A

; Patent No. 5790594

; GENERAL INFORMATION:

; APPLICANT: CARTER, DANIEL C.

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS

; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR

; TITLE OF INVENTION: RELATED PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NASA

; STREET: MARSHALL SPACE FLIGHT CENTER

; CITY: HUNTSVILLE

; STATE: ALABAMA

; COUNTRY: USA

; ZIP: 35812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/448,196A

RESULT 20

US-09-186-409-13

; Sequence 13, Application US/09186409

; Patent No. 5548629

; GENERAL INFORMATION:

APPLICANT: FARANO, Alessio

TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR

NUMBER OF SEQUENCES: 18

FILING DATE: 23-MAY-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: BROAD JR., ROBERT L.
 REGISTRATION NUMBER: 18,757
 REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 205-544-0258
 TELEX/FAX: 205-544-0258
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 583 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-448-196A-5
 Query Match 84.4%; Score 54; DB 1; Length 583;
 Best Local Similarity 81.8%; Pred. No. 0.033; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 1;
 Qy 1 DAKSEVAHRF 11
 Db 1 DTHKSHIAHRF 11

RESULT 22
 US-08-448-196A-6
 Sequence 6, Application US/08448196A
 Patent No. 5780594
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C.
 TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
 CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR RELATED PROTEINS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 STREET: MARSHALL SPACE FLIGHT CENTER
 CITY: HUNTSVILLE
 STATE: ALABAMA
 COUNTRY: USA
 ZIP: 35812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/803,364
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/_____
 FILING DATE: 20 FEB 1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A-6888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7000
 TELEX/FAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 US-08-803-364-6
 Query Match 78.1%; Score 50; DB 2; Length 13;
 Best Local Similarity 90.0%; Pred. No. 0.0028; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 1;
 Qy 3 HKGRBAHFRK 12
 Db 2 HKGRBAHFRK 11

RESULT 23
 US-08-803-364-6
 Sequence 6, Application US/08003364
 Patent No. 5864014
 GENERAL INFORMATION:
 APPLICANT: PASANO, Alessio
 TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MIKE, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/803,364
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A-6888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7000
 TELEX/FAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 US-08-803-364-6
 Query Match 78.1%; Score 50; DB 2; Length 13;
 Best Local Similarity 90.0%; Pred. No. 0.0028; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 1;
 Qy 3 HKGRBAHFRK 12
 Db 2 HKGRBAHFRK 11

RESULT 24
 US-09-024-198-12
 Sequence 12, Application US/09024198
 Patent No. 5912323
 GENERAL INFORMATION:
 APPLICANT: PASANO, Alessio
 TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MIKE, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 US-08-448-196A-6

CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/186,409
 FILING DATE: 5 NOV 1998
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A-6888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 12:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO

US-09-024-198-12

RESULT 25
 US-09-186-409-12
 Sequence 12, Application US/09186409
 Patent No. 594629

GENERAL INFORMATION:
 APPLICANT: PASANO, Alessio
 TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/186,409
 FILING DATE: 5 NOV 1998
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A-6888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO

US-09-186-409-12

Query Match 78.1%; Score 50; DB 2; Length 13;
 Best Local Similarity 90.0%; Pred. No. 0.0028; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

QY 3 HKSEVAHFRK 12
 ||||| |||||
 2 HKSEAAHFRK 11

RESULT 26
 US-09-803-364-1
 Sequence 1, Application US/09003364
 Patent No. 5864014

GENERAL INFORMATION:
 APPLICANT: PASANO, Alessio
 TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 CITY: Washington, D.C.
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/803,364
 FILING DATE: 20 FEB 1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A-6888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO

US-09-803-364-1

Query Match 78.1%; Score 50; DB 2; Length 16;
 Best Local Similarity 90.0%; Pred. No. 0.0035; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/024,198
 FILING DATE: 17 FEB 1998
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/803,364
 FILING DATE: 20 FEB 1997

QY 3 HKSEVAHRPK 12
 ; |||||
 ; Sequence 10, Application US/09024198
 ; Patent No. 5912323
 ; GENERAL INFORMATION:
 ; APPLICANT: FASANO, Alessio
 ; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 ; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 ; CITY: Washington, D.C.
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20037
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 PRIORITY DATA:
 APPLICATION NUMBER: 09/024,198
 FILING DATE: 17 FEB 1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: KIT, Gordon
 REFERENCE/DOCKET NUMBER: A-6988
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 US-09-186-409-10
 Query Match 78.1%; Score 50; DB 2; Length 16;
 Best Local Similarity 90.0%; Pred. No. 0.0035; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1;
 QY 3 HKSEVAHRPK 12
 Db 3 HKSEVAHRPK 12

RESULT 29
 US-09-041-774-1
 ; Sequence 1, Application US/08041774
 ; Patent No. 5550114
 ; GENERAL INFORMATION:
 ; APPLICANT: Strayer, David S.
 ; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR INHIBITOR
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/041,774
 FILING DATE: 19930402
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Zivin, No 5550114an H.
 REFERENCE/DOCKET NUMBER: 25,1985
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550

RESULT 28
 US-09-186-409-10
 ; Sequence 10, Application US/09186409
 ; Patent No. 5948629
 ; GENERAL INFORMATION:
 ; APPLICANT: FASANO, Alessio
 ; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 ; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 ; CITY: Washington, D.C.
 ; STATE: D.C.
 ; COUNTRY: U.S.A.

TELEFAX: (212) 977-9809
 TELEX: 422523 COOP UT
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: N
 ANTI-SENSE: N
 FRAGMENT TYPE: internal
 US-08-041-774-1

Query Match 75.0%; Score 48; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0048; Mismatches 1; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAH 10
 1 ||||:|||
 1 DTHKSEIAHR 10

RESULT 30

US-08-530-340-7
 Application US/08530340A
 Sequence 7, Patent No. 625532
 GENERAL INFORMATION:

APPLICANT: Strayer, David S
 TITLE OF INVENTION: Epidermal Growth Factor Inhibitor
 FILE REFERENCE: JEFF-0226
 CURRENT APPLICATION NUMBER: US/08/530,340A
 CURRENT FILING DATE: 1995-12-22
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 7

LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: An epidermal
 OTHER INFORMATION: growth factor inhibitor peptide
 US-08-530-340-7

Query Match 75.0%; Score 48; DB 4; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0048; Mismatches 1; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAH 10
 1 ||||:|||
 1 DTHKSEIAHR 10

RESULT 31

US-08-469-856-9
 Application US/08469856
 Sequence 9, Patent No. 5650307
 GENERAL INFORMATION:

APPLICANT: Sijmons, Peter C.
 APPLICANT: Hoekema, Andreas
 APPLICANT: Dekker, Bernardus M.M.
 APPLICANT: Schrammeijer, Barbara
 APPLICANT: Verwoerd, Tewniis C.
 TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS IN
 PLANTS AND PLANT CELLS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Avenue, NW, Ste. 5500
 CITY: Washington
 STATE: DC
 COUNTRY: USA

ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 OPERATING SYSTEM: PC-DOSS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/727,814B
 FILING DATE: 06-JUL-1990
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 4021571.7
 ATTORNEY/AGENT INFORMATION:
 NAME: Murray, Robert B.
 REGISTRATION NUMBER: 22,980
 REFERENCE/DOCKET NUMBER: 911014
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 659-2930
 TELEFAX: (202) 887-0357
 TELEX: 440142
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1288 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-727-814B-2

Query Match 67.2%; Score 43; DB 1; Length 1288;
 Best Local Similarity 66.7%; Pred. No. 8.2; Mismatches 0; Indels 4; Gaps 0;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 Db 577 DAHFEYGHFRK 588

RESULT 33
 US-08-258-614-2

Sequence 2, Application US/08258614
 Ent. No. 542070

GENERAL INFORMATION:
 APPLICANT: SCHUMACHER, Gunther
 APPLICANT: BURTSCHER, Helmut
 APPLICANT: MOLLERLING, Hans
 TITLE OF INVENTION: CLONED N-METHYLHYDANTOINASE
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nakaido, Marmelstein, Murray & Oram
 STREET: 655 Fifteenth Street N.W. Suite 330
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-5701

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/258,614
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/021,856
 FILING DATE: 24-FEB-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 40 21 571.7
 FILING DATE: 06-JUL-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/727,814
 FILING DATE: 08-JUL-1991

ATTORNEY/AGENT INFORMATION:
 NAME: KITTS, Monica C.
 REGISTRATION NUMBER: 36,105
 REFERENCE DOCKET NUMBER: P564-3007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5000
 TELEFAX: (202) 638-4810

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-258-614-2

Query Match 67.2%; Score 43; DB 1; Length 1288;
 Best Local Similarity 66.7%; Pred. No. 8.2; Mismatches 0; Indels 4; Gaps 0;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 Db 577 DAHFEYGHFRK 588

RESULT 34
 US-09-165-926-2

Sequence 2, Application US/09165926
 Patent No. 6461875

GENERAL INFORMATION:
 APPLICANT: Bar-Or, David
 APPLICANT: Lau, Edward
 APPLICANT: Winkler, James V.

TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit

FILE REFERENCE: ISCB5269-183196

CURRENT APPLICATION NUMBER: US/09/165,926
 CURRENT FILING DATE: 1998-10-02
 NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 2
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-165-926-2

Query Match 62.5%; Score 40; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVA 8
 Db 1 DAHKSEVA 8

RESULT 35
 US-09-171-461-28

Sequence 28, Application US/09171461
 Patent No. 6335016

GENERAL INFORMATION:
 APPLICANT: Baker, Adam
 APPLICANT: Cotten, Matthew
 APPLICANT: Chiocca, Susanna
 APPLICANT: Kurzbauer, Robert
 APPLICANT: Schaffner, Gotthold

TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus

FILE REFERENCE: 0652.1800000
 CURRENT APPLICATION NUMBER: US/09/171,461
 CURRENT FILING DATE: 1999-01-12
 EARLIER APPLICATION NUMBER: PCT/EP97/01944
 EARLIER FILING DATE: 1997-04-18
 NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 28
 LENGTH: 1121
 TYPE: PRT

ORGANISM: CELO VIRUS

FEATURE:
 OTHER INFORMATION: Position: 6501..9866/Product: E2b pol

US-09-171-461-28

Query Match 62.5%; Score 40; DB 4; Length 1121;
 Best Local Similarity 58.3%; Pred. No. 25; Mismatches 2; Indels 3; Gaps 0;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 Db 132 DSHPGEVARRR 143

RESULT 36
 US-08-738-168B-15

Sequence 15, Application US/08738168B
 Patent No. 6132988

GENERAL INFORMATION:
 APPLICANT: Sugino, Hiromu
 APPLICANT: Nakamura, Takanori

APPLICANT: Shouji, Hiroki
 TITLE OF INVENTION: NEURONAL CELL-SPECIFIC RECEPTOR PROTEIN
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/738,168B
 FILING DATE: 25-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 280939/1995
 FILING DATE: 27-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 174909/1996
 FILING DATE: 04-JUL-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 342/46901

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-738-168B-15

Query Match 59.4%; Score 38; DB 4; Length 514;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAHKSEVAHR 10
 Db 313 DGHKPAVHR 322

RESULT 37

#-134-001C-5307

Sequence 5307, Application US/09134001C
 Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 5307

LENGTH: 80
 TYPE: PPT
 ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5307

Query Match 56.2%; Score 36; DB 4; Length 80;
 Best Local Similarity 60.0%; Pred. No. 7.5;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 HKSEVAHRFK 12
 : ||| :|||
 14 NKKELAHR 23

RESULT 38

US-08-357-533A-11

Sequence 11, Application US/08357533A

PATENT NO. 5831050

GENERAL INFORMATION:

APPLICANT: JIN, DONALD F

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: SMART, JOHN E

TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/357,533A

FILING DATE: 16-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KELLY, ROBIN D

REGISTRATION NUMBER: 34,637

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)-435-9001

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 513 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:
 NAME/KEY: Protein

LOCATION: 1..513

OTHER INFORMATION: /note= "RAT ACTIVIN TYPE II

OTHER INFORMATION: RECEPTOR"

US-08-357-533A-11

Query Match 53.9%; Score 34.5; DB 2; Length 513;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAHKSEVAHR-FK 12

Db 312 EGHKPSIAHRDFK 324

RESULT 39

US-08-455-009-11

Sequence 11, Application US/08459009

PATENT NO. 5861479

GENERAL INFORMATION:

APPLICANT: JIN, DONALD F

APPLICANT: OPPERMANN, HERMANN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: SMART, JOHN E

TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
 STREET: 45 SOUTH STREET
 CITY: HOPKINTON
 STATE: MA
 COUNTRY: USA
 ZIP: 01748
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,009
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/357,533
 FILING DATE: 16-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: KELLY, ROBIN D
 REGISTRATION NUMBER: 34,637
 REFERENCE/DOCKET NUMBER: CRP-073FW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508)-435-9001
 TELEFAX: (508)-435-0992
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 513 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..513
 OTHER INFORMATION: /note= "RAT ACTIVIN TYPE II"
 OTHER INFORMATION: RECEPtor
 US-08-459-009-11
 Query Match 53.9%; Score 34.5; DB 2; Length 513;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Indels 1; Gaps 1;
 1 DAHKSEVAHR-FK 12
 :|||:|||||
 312 EGHKPSIAHDFK 324
 RESULT 40
 US-08-459-951-11
 Sequence 11, Application US/08459951
 Patent No. 6093547
 GENERAL INFORMATION:
 APPLICANT: JIN, DONALD F
 APPLICANT: OPPERMANN, HERMANN
 APPLICANT: KUBERASAMPATH, THANGAVEL
 APPLICANT: SMART, JOHN E
 TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
 STREET: 45 SOUTH STREET
 CITY: HOPKINTON
 STATE: MA
 COUNTRY: USA
 ZIP: 01748
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/357,533A
 FILING DATE: 16-DEC-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KELLY, ROBIN D
 REGISTRATION NUMBER: 34,637
 REFERENCE/DOCKET NUMBER: CRP-073FW
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)-435-9001
 TELEFAX: (508)-435-0992
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 536 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..536
 OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II"
 OTHER INFORMATION: RECEPTOR
 US-08-357-533A-12

Query Match 53.9%; Score 34.5; DB 2; Length 536;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02; 3; Indels 1; Gaps 1;
 Matches 7; Conservative 2; Mismatches 3; QY 1 DAHKSEVAHR-FK 12
 Db 335 EGHKPSIAHRDFK 347

RESULT 42
 US-08-459-009-12
 Sequence 12, Application US/08459009
 Patent No. 5661479
 GENERAL INFORMATION:
 APPLICANT: JIN, DONALD F
 APPLICANT: OPPERMANN, HERMANN
 APPLICANT: KUBERASAMPATH, THANGAVEL
 APPLICANT: SMART, JOHN E
 TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
 ADDRESSEE: INC
 STREET: 45 SOUTH STREET
 CITY: HOPKINTON
 STATE: MA
 COUNTRY: USA
 ZIP: 01748

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,009
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/357,533
 FILING DATE: 16-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: KELLY, ROBIN D
 REGISTRATION NUMBER: 34,637
 REFERENCE/DOCKET NUMBER: CRP-073FW

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508)-435-9001
 TELEFAX: (508)-435-0992
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 536 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..536
 OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II"
 OTHER INFORMATION: RECEPTOR

Query Match 53.9%; Score 34.5; DB 3; Length 536;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02; 3; Indels 1; Gaps 1;
 Matches 7; Conservative 2; Mismatches 3; QY 1 DAHKSEVAHR-FK 12
 Db 335 EGHKPSIAHRDFK 347

RESULT 43
 US-08-459-951-12
 Sequence 12, Application US/08459951
 Patent No. 6093547
 GENERAL INFORMATION:
 APPLICANT: JIN, DONALD F
 APPLICANT: OPPERMANN, HERMANN
 APPLICANT: KUBERASAMPATH, THANGAVEL
 APPLICANT: SMART, JOHN E
 TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
 ADDRESSEE: INC
 STREET: 45 SOUTH STREET
 CITY: HOPKINTON
 STATE: MA
 COUNTRY: USA
 ZIP: 01748

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,951
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/357,533
 FILING DATE: 16-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: KELLY, ROBIN D
 REGISTRATION NUMBER: 34,637
 REFERENCE/DOCKET NUMBER: CRP-073FW

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508)-435-9001
 TELEFAX: (508)-435-0992
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 536 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..536
 OTHER INFORMATION: /note= "HUMAN ACTIVIN TYPE II"
 OTHER INFORMATION: RECEPTOR

Query Match 53.9%; Score 34.5; DB 3; Length 536;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02; 3; Indels 1; Gaps 1;
 Matches 7; Conservative 2; Mismatches 3; QY 1 DAHKSEVAHR-FK 12
 Db 335 EGHKPSIAHRDFK 347

RESULT 44
US-08-586-039B-37
Sequence 37, Application US/08586039B
; Patent No. 6140073
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07045-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586, 039B
APPLICATION NUMBER: 07/676, 436
FILING DATE: 16-JAN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-586-039B-37
Query Match 53.1%; Score 34; DB 4; Length 138;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 3; Indels 0; Gaps 0;
; Mismatches 2;
Qy 1 DAHKSEVAHRF 11
Db 59 DEHPNEVSHIF 69
RESULT 45
US-09-173-30-34
Sequence 34, Application US/09173300
; Patent No. 6451581
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalaki, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 34
LENGTH: 210
TYPE: PRT
ORGANISM: Escherichia coli
US-09-173-300-34
Query Match 53.1%; Score 34; DB 4; Length 210;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
; Mismatches 1;
Qy 1 DAHKSEVAHR 10
Db 36 DSHKGVVRH 45

RESULT 45
US-08-586-039B-39
Sequence 39, Application US/08586039B
; Patent No. 6140073
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
APPLICANT: Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA

TELEPHONE: (508) 435-9001
 TELEFAX: (508) 435-0992
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 513 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..513
 OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"

US-08-459-009-10

Query Match 53.1%; Score 34; DB 2; Length 513;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Matches 5; Conservative
 Matches 5; Mismatches 2; Indels 3; Gaps 0;
 QY 1 DAHKSEVAHR 10
 Db 312 DGHKPAISHR 321

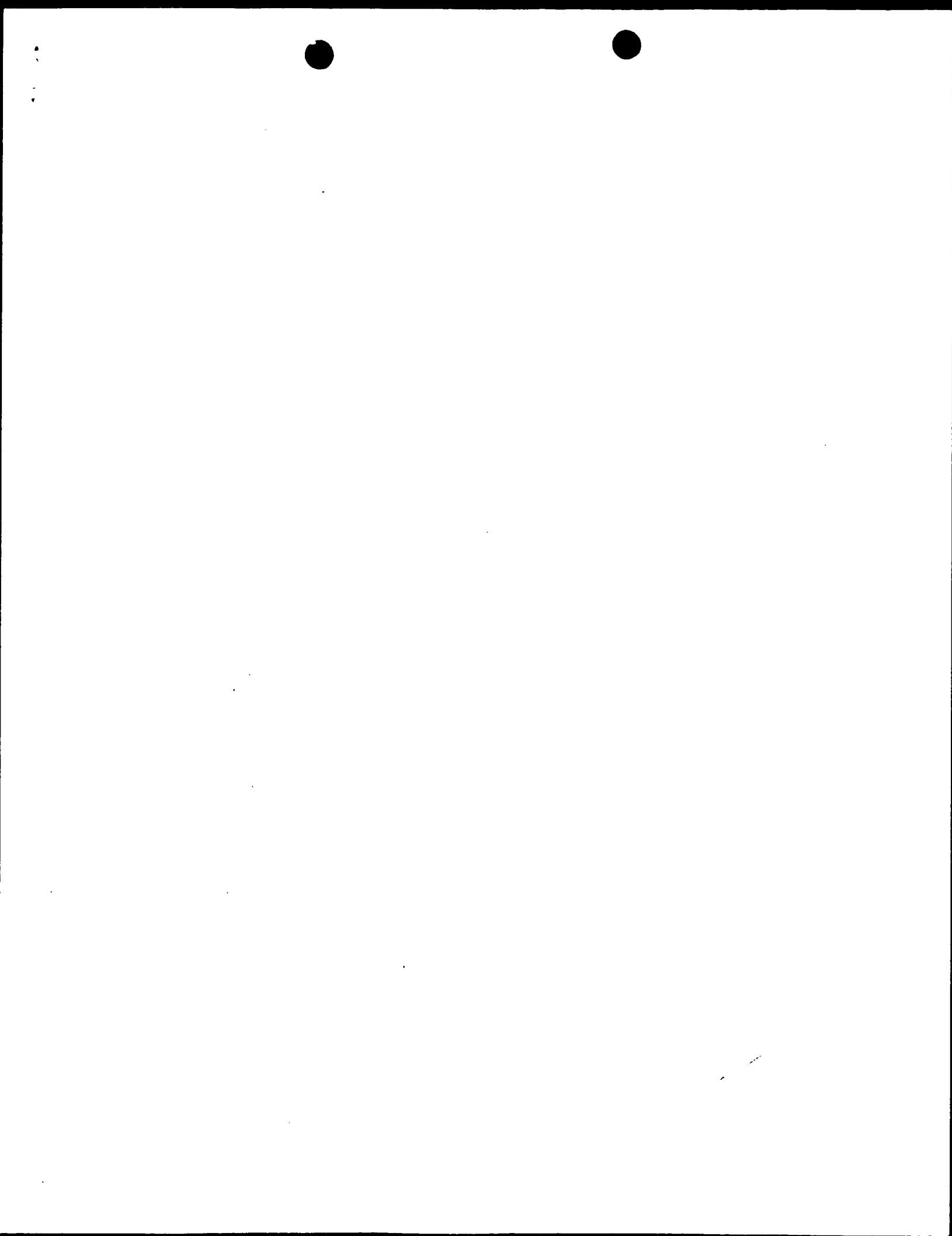
Search completed: April 11, 2003, 15:20:06
 Job time : 15 secs

QY	1 DAHKSEVAHR 10
Db	312 DGHKPAISHR 321

Query Match 53.1%; Score 34; DB 2; Length 513;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Matches 5; Conservative
 Matches 5; Mismatches 2; Indels 3; Gaps 0;

RESULT 50
 US-08-300-584-2
 Sequence 2, Application US/08300584
 Patent No. 5855794
 GENERAL INFORMATION:
 APPLICANT: Matthews, Lawrence S.
 APPLICANT: Vale, Wylie W.
 TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
 TITLE OF INVENTION: RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 STREET: 444 South Flower Street, Suite 2000
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/300,584
 FILING DATE: 02-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/880,220
 FILING DATE: 08-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/773,229
 FILING DATE: 09-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/698,709
 FILING DATE: 10-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Reiter, Stephen E.
 REGISTRATION NUMBER: 31,192
 REFERENCE/DOCKET NUMBER: P41 9806
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-546-1995
 TELEFAX: 619-546-9992
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 513 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 NAME/KEY: Protein
 LOCATION: 1..513
 OTHER INFORMATION: /note= "MOUSE ACTIVIN RECEPTOR"

US-08-300-584-2



- A;Residues: 1-120, 'G', 122-609 <DUG>
 A;Cross-references: EMBL:V00494; NID:92859; PIDN:CAA23753.1; PID:928590
 R;Uranio, Y.; Watabane, K.; Sakai, M.; Tamaoki, T.
 J;Bil. Chem. 261, 3244-3251, 1986
 A;Title: The human albumin gene. Characterization of the 5' and 3' flanking regions and
 A;Reference number: I19427; MUID:8810099; PMID:2419329
 A;Accession: I19427
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-26 <URA>
 A;Cross-references: GB:NM13075; NID:gi178330; PIDN:AA151688.1; PID:9553173
 R;Watkins, S.; Madison, J.; Galliano, M.; Minchietti, L.; Putnam, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994
 A;Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian family.
 A;Reference number: I159286; MUID:94181575; PMID:8134387
 A;Accession: I159286
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 282-290, 'KERRQDQ' <WAT>
 A;Cross-references: GB:SG69192; NID:gi546032; PIDN:AB30282.1; PID:9546033
 A;Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia
 J;Edison, J.; Galliano, M.; Watkins, S.; Minchietti, L.; Porta, F.; Rossi, A.; Putnam,
 Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994
 A;Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl-
 A;Reference number: I15313; MUID:94294404; PMID:8022807
 A;Accession: I15313
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 589-590, 'A|FRRVKNLQLQKLP' <MAD>
 A;Cross-references: GB:SG70799; NID:gi947231; PIDN:AAB31177.1; PID:9547232
 A;Note: this frame-shift variant is designated albumin Bazzano; four additional variants
 R;Menaya, J.; Parrilla, R.; Ayuso, M.S.
 Submitted to the EMBL Data Library, March 1995
 A;Reference number: G08292
 A;Accession: G01747
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-120, 'G', 122-455 <ME>
 A;Cross-references: EMBL:U229361; NID:gi763428; PIDN:AAA64922.1; PID:973431
 R;Edgerleyfood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
 Biochem. J. 321-325, 1995
 A;Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kex2
 A;Reference number: S55314; MUID:95275251; PMID:7755581
 A;Accession: S55314
 A;Molecule type: protein
 A;Residues: 19-27 <LED>
 A;Accession: S55314
 A;Molecule type: protein
 A;Residues: 19-27 <LED>
 R;Meloun, B.; Moravek, L.; Kostka, V.
 FEBS Lett. 58, 134-137, 1975
 A;Title: Complete amino acid sequence of human serum albumin.
 A;Reference number: I91420; MUID:76187907; PMID:1225573
 A;Accession: I91420
 A;Molecule type: protein
 A;Residues: 25-117, 'BQ', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-
 R;Rehr, U.; Spittel, G.; Trippel, D.
 Justus Liebigs Ann. Chem. 9, 881-884, 1988
 A;Title: Isolation and structure elucidation of middle-molecular weight peptides from ur
 A;Reference number: S06422
 A;Note: this paper is in German, with an English abstract
 A;Accession: S06422
 A;Molecule type: protein
 A;Residues: 25-48 <ROE>
 R;Finch, J.W.; Couch, R.K.; Knapp, D.R.; Schey, K.L.
 Arch. Biochem. Biophys. 305, 595-599, 1993
 A;Title: Mass spectrometric identification of modifications to human serum albumin treat
 A;Reference number: S36882; MUID:93384321; PMID:8373198
 A;Accession: S36882
 A;Molecule type: protein
 A;Residues: 45-67-160, 311-337, 469-490, 570-581 <FIN>
 R;Kausler, E.; Spittel, G.
 Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
 A;Title: Bruchstücke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
 A;Reference number: S17599; MUID:92126241; PMID:177598
 A;Accession: S17599
- A;Molecule type: protein
 A;Residues: 25-54;54-357;431-447 <KAU>
 A;Note: 49-Leu was also found
 R;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
 J;Immuno. 143, 1680-1684, 1989
 A;Title: Structures of histamine-releasing peptides formed by the action of acid protease
 A;Reference number: A45800; MUID:89341406; PMID:2474609
 A;Accession: A45800
 A;Molecule type: protein
 A;Residues: 166-173 <CAR>
 R;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Maj
 Biomed. Biophys. Res. Commun. 116, 983-988, 1986
 A;Title: The amino acid sequence of kinetinbin, a novel peptide isolated from pepsin-trea
 A;Reference number: A03239; MUID:86242180; PMID:3087352
 A;Accession: A03239
 A;Molecule type: protein
 A;Residues: 166-173, 'L' <MOG>
 R;Galliano, M.; Minchietti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
 A;Title: Mutations in genetic variants of human serum albumin found in Italy.
 A;Reference number: A38255; MUID:91062352; PMID:2247440
 A;Accession: C38255
 A;Molecule type: protein
 A;Residues: 76-111 <GALL>
 A;Accession: B38255
 A;Molecule type: protein
 A;Residues: 82-105, 'K' <107-110 <GALI2>
 A;Note: this variant is designated albumin Vibo Valentia
 R;Minchietti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
 Eur. J. Biochem. 214, 417-444, 1993
 A;Title: The structural characterization and bilirubin-binding properties of albumin Hert
 A;Reference number: S33928; MUID:93295054; PMID:8513793
 A;Accession: S33928
 A;Molecule type: protein
 A;Residues: 255-263, 'E' <265-281 <MINI>
 A;Note: this variant is designated albumin Herborn
 R;Minchietti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Porta,
 Biochim. Biophys. Acta 1119, 232-238, 1992
 A;Title: Two alloalbumins with identical electrophoretic mobility are produced by differ
 A;Reference number: S21078; MUID:92190239; PMID:1347703
 A;Accession: S21078
 A;Molecule type: protein
 A;Residues: 354-356, 'K' <358-378 <MIN2>
 A;Note: this variant is designated albumin Sondrio; another variant Paris-2 is reported,
 R;He, X.M.; Carter, D.C.
 Nature 358, 209-215, 1992
 A;Title: Atomic structure and chemistry of human serum albumin.
 A;Reference number: A46756; MUID:9233427; PMID:1630489
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms
 R;Brown, J.R.; Shockley, P.; Behrens, P.Q.
 In The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp 23-40,
 A;Reference number: A94422
 A;Contents: annotation; three-dimensional structure and disulfide bonds
 R;Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
 Collect. Czech. Chem. Commun. 42, 564-579, 1977
 A;Title: Disulfide bonds in human serum albumin.
 A;Reference number: A90930
 A;Contents: annotation; disulfide bonds
 R;Jacobsen, C.
 Biochem. J. 171, 453-459, 1978
 A;Title: Lysine residue 240 of human serum albumin is involved in high-affinity binding
 A;Reference number: A90299; MUID:78186630; PMID:656055
 A;Contents: annotation; bilirubin-binding site
 R;Peters, T.; Reed, R.G.
 in Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjoholm, I., eds., 11-20,
 A;Title: Serum albumin: conformation and active sites.
 A;Reference number: A94408
 A;Contents: annotation; binding sites
 R;Harper, M.B.; Dugaiczky, A.

Am. J. Hum. Genet. 35, 565-572, 1983
 A;Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
 A;Reference number: A46755; MUID:76257808; PMID:955075
 A;Contents: annotation
 R.Walter, J.E.
 FEBS Lett. 66, 173-175, 1976
 A;Title: Lysine residue 199 of human serum albumin is modified by acetylsalicylic acid.
 A;Reference number: A46294; MUID:92183881; PMID:154460
 A;Contents: annotation
 A;Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicylic acid
 R.Bohney, J.P.; Bonda, M.L.; Feldhoff, R.C.
 FEBS Lett. 298, 266-268, 1992
 A;Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phosphate
 A;Reference number: A56294; MUID:92183881; PMID:154460
 A;Contents: annotation
 A;Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; in P
 arabae activity
 C;Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized
 in liver, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak
 comment: A large number of variants of human serum albumin have been described.
 C;Genetic:
 A;Gene: GDB:ALB
 A;Cross-references: GDB:118990; OMIM:103600
 A;Map position: 4q11-4q13
 C;Superfamily: serum albumin; serum albumin repeat homology <SA1>
 C;Keywords: Carrier protein; duplication; metal binding; phosphoprotein; plasma; pyridox
 F:18-24/Domain: signal sequence #status predicted <SG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-60/Domain: product: serum albumin #status experimental <MPR>
 F:29-203/Domain: Serum albumin repeat homology <SA1> experimental <KIP>
 F:166-174/Domain: kinetensin #status experimental <KIP>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>
 F:27/Binding site: copper (His) #status predicted <PRO>
 F:77-85,9-115,114-125,148-193,201-224-201,224-277,289-303,302-313,340-385,384-393,
 F:214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
 Query Match 100.0% Score 64; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0 0.0077;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHRFK 12
 Db 25 DARKSEVAHRFK 36
 RESULT 2
 91 Human albumin precursor - rhesus macaque
 C;Species: Macaca mulatta (*rhesus macaque*)
 C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 C;Accession: A47391
 R;Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, B.; Smith, D.G.; Dwulet, J.; Putnam, P.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
 A;Title: cDNA and protein sequence of Polymorphic macaque albumins that differ in biliru
 A;Reference number: A47391; MUID:93211971; PMID:8846052
 A;Contents: B1B homozygote
 A;Accession: A47391
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 1-600 <WAT>
 A;Cross-references: GB:M90463; NID:9342294; PIDN:AAA36906.1; PID:9342295
 A;Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBIPI:128281)
 C;Superfamily: serum albumin; serum albumin repeat homology <SA1>
 F:21-194/Domain: serum albumin repeat homology <SA1>
 F:213-385/Domain: serum albumin repeat homology <SA2>
 F:405-584/Domain: serum albumin repeat homology <SA3>

A;Accession: A91458
A;Molecule type: protein
A;Residues: 25-41, 'H', 43-117, 'EQ', 120-179, 181-189, 'E', 191-194, 'A', 196-213, 'T', 215-288, 'E'
R;Brown, J.R.
Submitted to the Atlas' April 1975
A;Reference number: A95551
A;Accession: A94551
A;Molecule type: protein
A;Residues: 190-195
>
R;Brown, J.R.
Fed. Proc. 33, 1389, 1974
A;Contents: annotation; disulfide bonds
R;Werlen, R.C.; Oford, R.E.; Rose, K.
R;Bloch, J. 302, 907-911, 1994
A;Title: Preparation and characterization of novel substrates of insulin proteinase (EC
A;Reference number: S55232; MUID:95031935; PMID:7945219
A;Accession: S55232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 529-536;563-572 <WER>
C;KeyWords: carrier protein; copper binding; duplication; plasma
F;1-18/Domain: signal sequence #status experimental <PRO>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-607/Product: serum albumin #status experimental <SIG>
F;29-201/Domain: serum albumin repeat homology <SA1>
F;412-591/Domain: serum albumin repeat homology <SA2>
F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,4
Query Match 92.2%; Score 59; DB 1; Length 607;
Best Local Similarity 83.3%; Pred. No. 0.0064; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFK 12
Db 25 DTHKSEIAHRFK 36

RESULT 4

ABTS

N;Alternate name: preproalbumin

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-May-1979 #sequence revision 31-May-1979 #text change 22-Jun-1999

C;Accession: A93672; R92211; A91946; A91940; C45800; I57621; A02233

C;Reference number: A93872; MUID:81223722; PMID:7017712

A;Molecule type: mRNA

A;Residues: 1-608 <SR>

A;Cross-references: GB:V01222; GB:JU00698; NIDP:955627; PIDN:CAA24532.1; PID:955628

R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.

J;Biol. Chem. 252, 6846-6855, 1977

A;Title: Rat liver pre-albumin: complete amino acid sequence of the pre-piece. Analyse

A;Reference number: A92211; MUID:7249657; PMID:893447

A;Note: Cleavages during protein maturation

A;Accession: A92211

A;Molecule type: protein

A;Residues: 1-38 <STR>

R;Isemura, S.; Ikenaka, T.

J;Biochem. 83, 35-48, 1978

A;Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage

A;Reference number: A91946; MUID:78109429; PMID:564345

A;Accession: A91946

A;Molecule type: protein

A;Residues: 25-22 <S1>

R;Isemura, S.; Ikenaka, T.

J;Biochem. 79, 1183-1196, 1976

RESULT 5

ABHS

Berlin albumin precursor - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999

C;Accession: S06936

R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.

Nucleic Acids Res. 17, 1045, 1989

A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.

A;Accession number: S06936; MUID:90098888; PMID:2602160

A;Molecule type: mRNA

A;Residues: 1-607 <BRO>

A;Cross-references: EMBL:X17055; NID:91396; PIDN:CAA34903.1; PID:91397

C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, retinoid hormones (weak bonds with these hormones promote their transfer across the membrane).

C;Superfamily: serum albumin; serum albumin repeat homology

C;KeyWords: carrier protein; duplication; metal binding; plasma

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-24/Domain: propeptide #status predicted <PRO>

F;25-607/Product: serum albumin #status predicted <MAT>

F;29-201/Domain: serum albumin repeat homology <SA1>

F;220-293/Domain: serum albumin repeat homology <SA2>

F;412-591/Domain: serum albumin repeat homology <SA3>

F;27/Binding site: copper (His) #status predicted

P;77-86,99-115,114-125,147-192,191-200,223-260,268-276,288-302,301-312,339-384,383-392,4
P;263/Binding site: bilirubin (Lys) #status predicted

Query Match 84.4%; Score 54; DB 1; Length 607;
Best Local Similarity 81.8%; Pred. No. 0 053; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRF 11
Db 25 DTHKSEIAHRF 35

RESULT 6

AH05
AB05
serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Accession: S34053
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
R;HO, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
A;Reference number: S34053; MUID:93345495; PMID:8344282
A;Accession: S34053
A;Molecule type: mRNA
A;Residues: 1-607 <HO>
C;Cross-references: GB:X74045; NID:9399671; PIDN:CAA52194_1; PID:9399672
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, steroid hormones (weak bonds with these hormones promote their transfer across the membrane) and its acid hydrolysis peptides dominate preparations of mineral. C;Superfamily: serum albumin repeat homology <SA1>
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: serum albumin #status predicted <MAT>
F;29-301/Domain: serum albumin repeat homology <SA1>
F;220-353/Domain: serum albumin repeat homology <SA1>
F;412-591/Domain: serum albumin repeat homology <SA1>
F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,147-192,191-200,223-260,268-276,288-302,301-312,339-384,383-392,4
F;263/Binding site: bilirubin (Lys) #status predicted

Query Match 84.4%; Score 54; DB 1; Length 607;
Best Local Similarity 81.8%; Pred. No. 0 053; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRF 11
Db 25 DTHKSEIAHRF 35

RESULT 7

JCS838
albumin - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Accession: JCS838
C;Date: 05-Mar-1998 #sequence_change 19-May-2000
R;Yoshida, K.; Sero-Oshima, A.; Sinohara, H.
DNA Res. 4, 351-354, 1997
A;Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in the
A;Reference number: JCS838; MUID:98116663; PMID:9455485
A;Accession: JCS838
A;Molecule type: mRNA
A;Residues: 1-609 <YOS>
A;Cross-references: DDBJ:AB006197; NID:92317277; PIDN:BA21765_1; PID:92317278
A;Experimental source: liver
C;Superfamily: serum albumin repeat homology <SA2>
F;222-335/Domain: serum albumin repeat homology <SA2>

Query Match 84.4%; Score 54; DB 2; Length 609;
Best Local Similarity 81.8%; Pred. No. 0 053; 2; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AHKSEVAHRFK 12
Db 25 DTHKSEIAHRFK 35

Db 27 AHKSEIAHRYK 37

RESULT 8

ABPGS
serum albumin precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S01382; S61006
R;Weinstock, J.; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Title: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:3174440
A;Accession: S01382
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-605 <WEI>
A;Cross-references: EMBL:X12422; NID:91875; PIDN:CAA30970_1; PID:9833798
R;Limback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
J. Bone Miner. Res. 4, 235-241, 1989
A;Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mineral.
A;Reference number: A61006; MUID:89269769; PMID:2728927
A;Accession: A61006
A;Molecule type: protein
A;Residues: 23-51, 'X', 53-54, 'XXXW', 146, 'E', 148, 'E', 150-151, 'XWN', 155 <LM>
A;Experimental source: dental enamel
A;Comment: albumin and other serum proteins are also found in bone
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, steroid hormones (weak bonds with these hormones promote their transfer across the membrane) and its acid hydrolysis peptides dominate preparations of mineral.
C;Superfamily: serum albumin repeat homology <SA1>
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-22/Domain: propeptide #status predicted <PRO>
F;23-605/Product: serum albumin #status predicted <MAT>
F;27-191/Domain: serum albumin repeat homology <SA1>
F;218-391/Domain: serum albumin repeat homology <SA2>
F;410-589/Domain: serum albumin repeat homology <SA2>
F;75-84, 97-113, 112-123, 145-190, 199-198, 221-267, 266-274, 286-300, 299-310, 337-382, 381-390, 41
F;261-394/Domain: bilirubin (Lys) #status predicted

Query Match 82.8%; Score 53; DB 1; Length 605;
Best Local Similarity 80.5%; Pred. No. 0 051; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFK 12
Db 23 DTYKSEIAHRFK 34

RESULT 9

JSS732
serum albumin precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Accession: JSS732
C;Date: 15-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
R;Hilger, C.; Grigioni, F.; Hentges, F.
Gene 169, 295-296, 1996
A;Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A;Reference number: JC4660; MUID:96194824; PMID:8647469
A;Accession: JC4660
A;Molecule type: mRNA
A;Residues: 1-508 <HT2>
A;Cross-references: EMBL:X84942; NID:9886484; PIDN:CAA59279_1; PID:9886485
A;Experimental source: liver
C;Comment: This protein is the major protein component in plasma. It functions as a multi-chain has 35 conserved cysteine residues.
C;Superfamily: serum albumin; serum albumin repeat homology <SA1>
C;Keywords: liver; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-608/Product: serum albumin #status predicted <MAT>
F;29-202/Domain: serum albumin repeat homology <SA2>
F;221-394/Domain: serum albumin repeat homology <SA2>

F:413-592/Domain: serum albumin repeat homology <SA3>
 Query Match 78.1%; Score 50; DB 2; Length 608;
 Best Local Similarity 72.7%; Pred. No. 0.29; Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRF 11
 :||:|||:
 Db 25 EAHQSEVAHRF 35

RESULT 10
 B61511
 serum albumin, milk-derived - Australian echidna (fragment)
 C;Species: *Tachyglossus aculeatus* (Australian echidna)
 C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
 C;Accession: B61511
 R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
 Comp. Biochem. Physiol. B 99, 99-118, 1991
 A;Title: Some monotreme milk "whey" and blood proteins.
 A;Reference number: A61511; MUID:92070088; PMID:1959333

A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-30 <GRI>
 C;Superfamily: serum albumin; serum albumin repeat homology
 C;Keywords: milk

Query Match 71.9%; Score 46; DB 2; Length 30;
 Best Local Similarity 66.7%; Pred. No. 0.068; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFK 12
 :|||:|||:
 Db 1 DAQKSELGHRYK 12

RESULT 11
 S29749
 serum albumin - dog
 C;Species: *Canis lupus familiaris* (dog)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C;Accession: S29749
 R;Dixon, J.W.; Sarkar, B.
 J. Biol. Chem. 249, 5872-5877, 1974
 A;Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-
 A;Reference number: S29749; MUID:75011422; PMID:4414013
 A;Accession: S29749
 R;Status: preliminary
 C;Molecule type: protein
 A;Residues: 1-12 <DIX>
 C;Superfamily: serum albumin; serum albumin repeat homology
 Query Match 70.3%; Score 45; DB 2; Length 24;
 Best Local Similarity 63.6%; Pred. No. 0.083; Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRF 11
 :|||:|||:
 Db 1 EAHKSEVAHRY 11

RESULT 12
 ABCS
 serum albumin precursor - chicken
 C;Species: *Gallus gallus*
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C;Accession: S15571; A0578; A13451
 R;Casady, A.I.; Skikild, C.K.; Baverstock, P.; Wallace, J.C.
 Submitted to the EMBL Data Library, July 1991
 A;Accession number: S15571
 A;Molecule type: mRNA

Query Match 61.7%; Score 39.5; DB 2; Length 201;
 Best Local Similarity 52.6%; Pred. No. 7.7; Matches 10; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 3 HKSEVAHRF 12
 :|||:
 Db 79 HKKSSLYVTDDEVAHRFK 97

RESULT 13
 E82910
 hypothetical protein UU287 [imported] - *Ureaplasma urealyticum*
 C;Species: *Ureaplasma urealyticum*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: E82910
 R;Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a mini
 A;Reference number: AB2870
 A;Accession: E82910
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1201 <GLA>
 A;Cross-references: GB:AE002125; GB:AF222894; NID:96899253; PIDN:AAF30696.1; GSPDB:GN001;
 A;Experimental source: serovar 3; biovar 1
 A;Genetics: UU287
 A;Genetic code: SGC3

Query Match 61.7%; Score 39.5; DB 2; Length 201;
 Best Local Similarity 52.6%; Pred. No. 7.7; Matches 10; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 3 HKSEVAHRF 12
 :|||:
 Db 79 HKKSSLYVTDDEVAHRFK 97

RESULT 14
 AH2378
 hypothetical protein asr4584 [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp.
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AH2378
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sabamoto, S.; Watanabe, A.; Iriuchii, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120
A;Reference number: AB1807; MUID:2195285; PMID:11759840
A;Accession: AH2378
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-93 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76283.1; PID:917133720; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Gene: agr4584
Db 44 NTHAAADVahrF 54

RESULT 15

Query Match Score 59.4%; DB 2; Length 93;
Best Local Similarity 54.5%; Pred. No. 66; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 DAHKSEVAHR 11
: : ||||| :|||

S21171 activin receptor STK9 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 28-Feb-1997
C;Accession: S21171
R;Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N.
FBS Lett. 303, 81-84, 1992
A;Title: Multiple genes for Xenopus activin receptor expressed during early embryogenesis
A;Reference number: S21171; MUID:92275088; PMID:1317302
A;Accession: S21171
A;Molecule type: mRNA
A;Residues: 1-512 <NIS>
C;Superfamily: activin receptor II; protein kinase homology
C;Keywords: ATP
F,189-485/Domain: protein kinase homology <KIN>

Query Match Score 59.4%; DB 2; Length 512;
Best Local Similarity 70.0%; Pred. No. 39; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHR 10
: : ||||| :|||

S21171 activin receptor precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C;Accession: JQ0317
R;Kondo, M.; Tashiro, K.; Fujii, G.; Asano, M.; Miyoshi, R.; Yamada, R.; Muramatsu, M.; Bloch, M.; Biophys. Res. Commun. 181, 684-690, 1991
A;Title: Activin receptor mRNA is expressed early in Xenopus embryogenesis and the level of expression is increased during development
A;Reference number: JQ0317; MUID:92095974; PMID:1661587
A;Accession: JQ0317
A;Molecule type: mRNA
A;Residues: 1-514 <KON>
A;Cross-references: GB:ST0930; PIDN:AAB20638.1; PID:9240782
C;Superfamily: activin receptor II; protein kinase homology; transmembrane
C;Keywords: ATP; glycoprotein; serine/threonine-specific protein kinase; transmembrane
C;Keywords: F1-20/Domain: signal sequence #status predicted <SIG>
F,21-514/Product: activin receptor #status predicted <ACT>
F,37-162/Domain: transmembrane #status predicted <TRA>
F,191-487/Domain: protein kinase homology <KIN>
F,46, 67, 88, 214, 334/Binding site: carbohydrate (asn) (covalent) #status predicted

RESULT 16

Query Match Score 59.4%; DB 2; Length 489;
Best Local Similarity 50.0%; Pred. No. 56; Indels 4; Gaps 1;
Matches 8; Conservative 4; Mismatches 0; Indels 4; Gaps 1;

Qy 1 DAHKS---EVahrF 12
: : ||| : : |||||

T12251 sucrose synthase (EC 2.4.1.13) - common ice plant (fragment)
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 02-Jun-2000
C;Accession: T12251
R;Michałowski, C.B.; Bonnett, H.J.
Submitted to the EMBL Data Library, March 1998
A;Description: An expressed sequence tag for sucrose synthase from *M. crystallinum*.
A;Reference number: Z17473
A;Accession: T12251
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-67 <MIC>
A;Cross-references: EMBL:AF024446; NID:93064040; PID:93064041
C;Superfamily: sucrose synthase; sucrose/acrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase
Query Match Score 56.2%; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 11; Indels 4; Gaps 0;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHR 12
: : ||| : : |||

RESULT 17

Query Match Score 38; DB 2; Length 514;
Best Local Similarity 70.0%; Pred. No. 39; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHR 10
: : ||| : |||

Db 313 DGHKPAVahr 322

RESULT 18

Query Match Score 57.8%; DB 2; Length 489;
Best Local Similarity 50.0%; Pred. No. 56; Indels 4; Gaps 1;
Matches 8; Conservative 4; Mismatches 0; Indels 4; Gaps 1;

Qy 1 DAHKS---EVahrF 12
: : ||| : : |||||

Db 276 BANKALVSREBIahrF 291

RESULT 19

Query Match Score 37; DB 2; Length 489;
Best Local Similarity 50.0%; Pred. No. 56; Indels 4; Gaps 1;
Matches 8; Conservative 4; Mismatches 0; Indels 4; Gaps 1;

T30740 hypothetical protein 138R - *Molluscum contagiosum* virus 1
N;Alternative names: MC138R
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000

C;Accession: T30740
 R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
 A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
 A;Reference number: Z220876; MUID:96325459; PMID:8670425
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residues: 1-117 <SEN>
 A;Cross-references: EMBL:U60315; PIDN: AAC55266.1
 C;Genetics:
 A;Note: MC138R
 C;Superfamily: variola major virus 6R protein
 Query Match 56.2%; Score 36; DB 2; Length 117;
 Best Local Similarity 77.8%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AHKSEVAHR 10
 Db 24 AHKSFAHHR 32

RESULT 20
 F83532
 conserved hypothetical protein PA0915 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: F83532
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: F83532
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-153 <STO>
 A;Cross-references: GB:AE004525; GB:AE004091; NID:99946805; PIDN:AAG04304.1; GSPDB:GN001
 C;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA0915
 Query Match 56.2%; Score 36; DB 2; Length 153;
 Best Local Similarity 63.6%; Pred. No. 26; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 DHAKSEVAHRF 11
 Db 18 DAHLAELAHRF 28

RESULT 21
 B84870
 probable molybdopterin synthase large subunit [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: B84870
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Li
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vaniken, S.E.; Umayam, L.; Tallon, J.
 Eubs, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: B84870
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residue: 1-198 <STO>
 A;Cross-references: GB:AE002093; NID:92281094; PIDN:AAB64030.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: Atg43760
 A;Map position: 2

Query Match 56.2%; Score 36; DB 2; Length 198;
 Best Local Similarity 70.0%; Pred. No. 34; Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAHR 10
 Db 79 DIHKLAVAHR 88

RESULT 22
 T02888
 thymidine kinase (EC 2.7.1.21) [similarity] - rice
 C;Species: *Oryza sativa* (rice)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jun-2002
 C;Accession: T02888
 R;Ullah, H.; Robertson, N.; Fitts, R.C.
 submitted to the EMBL Data Library, May 1998
 A;Description: Plant thymidine kinase.
 A;Reference number: Z14763
 A;Accession: T02888
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-212 <URL>
 A;Cross-references: EMBL:AT066050; NID:93411151; PID:g3411152
 A;Experimental source: cultivar Nippobare
 C;Genetics:
 A;Gene: TK
 C;Superfamily: *Escherichia coli* thymidine kinase
 C;Keywords: ATP; DNA biosynthesis; phosphotransferase
 Query Match 56.2%; Score 36; DB 2; Length 212;
 Best Local Similarity 58.3%; Pred. No. 36; Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAHRFK 12
 Db 201 DLEKSKVHAFK 212

RESULT 23
 B70379
 dihydrodipicolinate reductase - *Aquifex aeolicus*
 C;Species: *Aquifex aeolicus*
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
 C;Accession: B70379
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
 V.; Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: B70379
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-265 <AQF>
 A;Cross-references: GB:AE000713; NID:92983424; PIDN:AAC07008.1; PID:92983426; GB:AE000655
 A;Experimental source: strain VR5
 C;Genetics:
 A;Gene: dapB
 C;Superfamily: dihydrodipicolinate reductase
 Query Match 56.2%; Score 36; DB 2; Length 265;
 Best Local Similarity 58.3%; Pred. No. 45; Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAHRFK 12
 Db 151 DASIMEIHRFK 162

RESULT 24
 T42407
 gephyrin homolog - *Caenorhabditis elegans*

Db 67 HKKKVVAHR 74

RESULT 29

D96750

unknown protein F28P22.22 [imported] - *Arabidopsis thaliana* (mouse-ear cress)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: D96750

R.Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anseen, N.F.; Hughes, B.; Huizar, I.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Walker, M.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Cross-references: AB6141; MUID:21016719; PMID:11130712

A;Accession: D96750

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-320 <STO>

A;Cross-references: GB:AE005173; NID:96648169; PIDN:AAF21169.1; GSPDB:GN00141

A;Genetics:

A;Gene: F28P22.22

A;Map position: 1

Query Match 54.7%; Score 35; DB 2; Length 320;

Best Local Similarity 60.0%; Pred. No. 84; Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 HKSEVAHFRK 12
Db 100 HMTVHEHFRK 109

RESULT 30

I61180

nFB protein - *Haemophilus influenzae* (strain Rd KW20)

C;Species: *Haemophilus influenzae*

C;Accession: 18-Aug-1995 #sequence_revision 26-Jul-1996 #text_change 11-Jun-1999

R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Boccardo, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; Gocayne, J.D.; Brandau, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghegan, N.S.M.; Dice, 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.; Arntzen, Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: I61180

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-321 <TIGR>

A;Cross-references: GB:U32797; GB:L42023; NID:91574619; PIDN: AAC22724.1; PID:91574620; T

C;Genetics:

A;Gene: nrfd

C;Function:

A;Description: probably involved in the transfer of electrons from the quinone pool to t

C;Superfamily: nrfd protein

C;Keywords: transmembrane protein

A;Note: named as homolog to a protein from *Escherichia coli*

F130-146/Domain: transmembrane #status predicted <TMW1>

F1305-321/Domain: transmembrane #status predicted <TMW2>

Query Match 54.7%; Score 35; DB 1; Length 321;

Best Local Similarity 41.7%; Pred. No. 85; Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHFRK 12
Db 100 HMTVHEHFRK 109

Db 212 DSHESHFIHKPE 223

RESULT 31

S43415

histidine ammonia-lyase (EC 4.3.1.3) - human

C;Alternate names: histidase

C;Species: *Homo sapiens* (man)

C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999

C;Accession: S43415

R.Suchi, M.; Harada, N.; Wada, Y.; Takagi, Y.

Biochim. Biophys. Acta 1216, 293-295, 1993

A;Title: Molecular cloning of a cDNA encoding human histidase.

A;Reference number: S43415; MUID:94060103; PMID:7916645

A;Accession: S43415

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-657 <SUC>

A;Cross-references: DBu:D16626; NID:9451209; PIDN:BAA04047.1; PID:9451210

A;Genetics:

A;Gene: GDB:HAU; MHS

A;Cross-references: GDB:120746; OMIM:235800

A;Map position: 12q22-12q23

C;Function:

A;Description: catalyzes the formation of (E)-3-(1H-imidazol-4-yl)-propenoic acid (urocar

A;Pathway: histidine catabolism

C;Superfamily: histidine ammonia-lyase

C;Keywords: ammonia-lyase; carbon-nitrogen lyase; histidine catabolism

F;253-255/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted

F;254/Modified site: dehydroalanine (Ser) #status predicted

Query Match 54.7%; Score 35; DB 2; Length 657;

Best Local Similarity 61.5%; Pred. No. 1.8e+02; Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DAHKSEVAHFRK 11
Db 375 DHHPSEIAESHRF 387

RESULT 32

A36087

histidine ammonia-lyase (EC 4.3.1.3) - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 23-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Dec-1999

C;Accession: A36087

R.Taylor, R.G.; Lambert, M.A.; Sexsmith, E.; Sadler, S.J.; Ray, P.N.; Mathuran, D.J.; McIn

J.; Biol. Chem. 265, 18192-18199, 1990

A;Title: Cloning and expression of rat histidase. Homology to two bacterial histidases at

A;Reference number: A36087; MUID:9109306; PMID:2120224

A;Accession: A36087

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-657 <TAY>

A;Cross-references: GB:M58308; GB:J06653; NID:9204556; PIDN:AAA63491.1; PID:9204557

C;Superfamily: histidine ammonia-lyase

C;Keywords: ammonia-lyase; carbon-nitrogen lyase; histidine catabolism

F;253-255/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted

F;254/Modified site: dehydroalanine (ser) #status predicted

Query Match 54.7%; Score 35; DB 2; Length 657;

Best Local Similarity 61.5%; Pred. No. 1.8e+02; Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DAHKSEVAHFRK 11
Db 375 DHHPSEIAESHRF 387

RESULT 33

A46128

histidine ammonia-lyase (EC 4.3.1.3) - mouse

QY 1 DAHKSEVAHFRK 12

C;Species: *Mus musculus* (house mouse)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
 C;Accession: A46128
 R;Taylor, R.G.; Grieco, D.; Clarke, G.A.; McInnes, R.R.; Taylor, B.A.
 Genomics 16, 231-240, 1993
 A;Title: Identification of the mutation in murine histidinemia (his) and genetic mapping
 A;Reference number: A46128; MUID:93252384; PMID:8486363
 A;Accession: A46128
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-657 <TR>
 A;Cross-references: GB:L07645; NID:9193751; PIDN:AAA37777.1; PID:9193752
 A;Experimental source: C5BL
 A;Note: sequence extracted from NCBI backbone (NCBIN:131641, NCBIPI:131644)
 C;Function:
 A;Description: catalyzes the formation of (E)-3-(1H-imidazol-4-yl)-propenoic acid (uroca
 A;Pathway: histidine catabolism
 C;Superfamily: histidine ammonia-lyase
 C;Keywords: ammonia-lyase; carbon-nitrogen lyase; histidine catabolism
 C;25/5/Cross-link: 5-imidazoline (ala-Gly)
 A;Modified site: dehydroalanine (Ser) #status predicted

Query Match
 Best Local Similarity 54.7%; Score 35; DB 2; Length 690;
 Matches 8; Conservative 61.5%; Pred. No. 1.9e+02;
 Qy 1 DAHKSEVHFK 11
 Db 375 DHHPSEBIAESHRP 387

RESULT 34
 H82143 methyly-accepting chemotaxis protein VC1898 [imported] - *Vibrio cholerae* (strain NI6961) e
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: H82143
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardon, D.; Brimble, M.D.; Vamathevan, J.; Baldwin, S.; Qin, H.; Dragoi, I.; Sellers, E.
 L., R.R.; Makalowski, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: H82143
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-749

 A;Cross-references: EMBL:288977; PIDN:CA811656.1; GSPDB:GN00066; SPDB:SPAC23H4.01c
 A;Experimental source: strain 972h-; cosmid C23H4
 C;Genetics:
 A;Gene: SPDB:SPAC23H4_01c
 A;Map position: 1

Query Match
 Best Local Similarity 54.7%; Score 35; DB 2; Length 749;
 Matches 8; Conservative 66.7%; Pred. No. 2e+02; 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DAHKSEVHFK 12
 Db 403 DATKSSVHNEK 414

RESULT 35
 T22556 hypothetical protein K03A11.1 - *Caenorhabditis elegans* b
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1993 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T22556
 R;Swinburne, J.
 submitted to the EMBL Data Library, July 1996
 A;Reference number: Z1.9717
 A;Accession: T22556
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-969 <WIL>
 A;Cross-references: EMBL:277133; PIDN:CA800865.1; GSPDB:GN00028; CBSP:K03A11.1
 A;Experimental source: clone K03A11
 C;Genetics:
 A;Gene: CESP:K03A11.1
 A;Map position: X
 A;Gene: CESP:K03A11.1
 A;Map position: X
 A;Intron: 33/1; 116/1; 162/1; 185/1; 256/2; 359/1; 494/1; 580/1; 738/3; 765/3; 804/3; 84
 B42554 D-amino acid hydantoin hydrolase (ATP-hydrolyzing) (EC 3.5.2.-) hyua [validated] - Pseud
 C;Species: *Pseudomonas* sp.
 C;Accession: B42554
 C;Date: 01-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-2001
 R;Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
 J;Bacteriol. 174, 962-969, 1992
 A;Title: Cloning and sequencing of the genes involved in the conversion of 5-substituted
 A;Reference number: A42554; MUID:93121137; PMID:1732229
 A;Accession: B42554

Query Match
 Best Local Similarity 54.7%; Score 35; DB 2; Length 969;
 Matches 6; Conservative 54.5%; 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AHKSEVAHRPK 12
 Db 187 AHNSCAGYK 197

RESULT 38

T18552
Saframycin Mx1 synthetase A - *Myxococcus xanthus*
C;Species: *Myxococcus xanthus*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
C;Accession: T18552
R;Postleth. A.; Bietenhader, J.; Schupp, T.
Microbiol. 142, 741-746, 1996
A;Title: Two multifunctional peptide synthetases and an O-methyltransferase are involved
A;Reference number: 218967; MUID:97090395; PMID:8936303
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-2605 <POS>
A;Cross-references: EMBL:U24657; NID:gi171127; PID:gi171129; PIDN: AAC44129.1
C;Genetics:
A;Gene: safa
C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
C;Keywords: carrier protein
C;Species: acetyl-CoA ligase homology <ACT1>
C;Date: 5-978/Domain: acyl carrier protein homology <ACP1>
F11643-2091/Domain: acetyl-CoA ligase homology <ACT2>
F;2110-2178/Domain: acyl carrier protein homology <ACP2>

Query Match Score 54.7%; Score 35; DB 2; Length 2605;
Best Local Similarity 41.7%; Pred. No. 7.5e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFK 12
Db 1629 DAHANOLAHHLR 1640

RESULT 39

P04261
activin type II receptor - baboon (fragment)
C;Species: *Papio* sp. (baboon)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Aug-1997
C;Accession: PC4261
R;Zhao, Y.; Silbajoris, R.; Young, S.L.
Bloch, M.; Biophys. Res. Commun. 229, 56-57, 1996
A;Title: Identification and developmental expression of two activin receptors in baboon
A;Reference number: PC4260; MUID:97112402; PMID:8954082
A;Contents: lung
A;Accession: PC4261
A;Molecule type: mRNA
A;Residues: 1-251 <ZHA>
B;Residues references: GB:U60421
Comment: This protein plays a role in lung development and involved in transforming gr
C;Superfamily: activin receptor II; protein kinase homology (fragment) <KIN>
F;1-251/Domain: protein kinase homology (fragment) <KIN>

Query Match Score 53.9%; Score 34.5; DB 2; Length 251;
Best Local Similarity 53.8%; Pred. No. 81;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 DAHKSEVAHR-FK 12
Db 98 EGHKPSIAHRDFK 110

RESULT 40

B49193
Type II activin receptor ActRIIB - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: B49193
R;Feng, Z.M.; Madigan, M.B.; Chen, C.L.
Endocrinology 132, 2593-2600, 1993
A;Title: Expression of type II activin receptor genes in the male and female reproductive system
A;Reference number: A49193; MUID:9327247; PMID:7916881
A;Accession: B49193

RESULT 41

S62266
protein disulfide-isomerase (EC 5.3.4.1) - castor bean
C;Species: *Ricinus communis* (castor bean)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C;Accession: S62266
R;Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.
Eur. J. Biochem. 235, 215-224, 1996
A;Title: Molecular characterisation of plant endoplasmic reticulum: identification of protein disulfide-isomerase; thioredoxin homology
A;Reference number: S62620; MUID:96202938; PMID:8631332
A;Accession: S62626
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-498 <COU>
A;Cross-references: EMBL:U41385; NID:gi134967; PIDN: AAB05641.1; PID:gi134968
C;Superfamily: protein disulfide-isomerase; thioredoxin homology
C;Keywords: intramolecular oxidoreductase; isomerase
F;40-128/Domain: thioredoxin homology <TXN>

Query Match Score 53.9%; Score 34.5; DB 2; Length 498;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
Qy 1 DAHKS--EVAKRK 12
Db 284 DSIKSKYQEVAKRK 298

RESULT 42

B40829
activin receptor isoform IIB4 - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
C;Accession: B40829
R;Attisano, L.; Wran, J.L.; Cheifetz, S.; Massague, J.
Cell 68, 97-108, 1992
A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate a
A;Reference number: A40829; MUID:9211972; PMID:1310075
A;Accession: B40829
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-504 <ATP>
A;Experimental Source: Balb/c 3T3
A;Note: sequence inconsistent with the nucleotide translation
C;Superfamily: activin receptor II; protein kinase homology
C;Keywords: ATP; receptor
F;180-477/Domain: protein kinase homology <KIN>

Query Match Score 53.9%; Score 34.5; DB 2; Length 504;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 DAHKSEVAHR-FK 12
Db 303 EGHKPSIAHRDFK 315

RESULT 43
 activin receptor isoform :IB2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: D40829 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
 R;Rattisano, L.; Wrama, J.L.; Cheifetz, S.; Massague, J.
 Cell 68, 97-108, 1992
 A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate
 A;Reference number: A40829; MUID:92119722; PMID:1310075
 A;Accession: D40829
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-512 <ATT>
 A;Experimental source: Balb/c 3T3
 A;Note: sequence inconsistent with the nucleotide translation
 A;Keywords: ATP; receptor kinase homology <KIN>
 Query Match 53.9%; Score 34.5; DB 2; Length 513;
 Best Local Similarity 53.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 F;188-485/Domain: protein kinase homology <KIN>
 Qy 1 DAHKSEVAHR-FK 12
 Db 311 BGHKPSIAHDFK 323

RESULT 44
 activin type II receptor - human
 C;Species: Homo sapiens (man)
 C;Accession: I37134 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
 R;Hilzen, K.; Tauri, T.; Bramaa, M.; Ritvos, O.
 Blood 83, 2163-2170, 1994
 A;Title: Expression of type II activin receptor genes during differentiation of human K5
 A;Reference number: I37134; MUID:9414127; PMID:8361782
 A;Accession: I37134
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-512 <RSS>
 A;Cross-references: EMBL:X77533; NID:9825619; PIDN:CAA54671.1; PID:9825620
 B-485/Domain: protein kinase homology <KIN>
 Query Match 53.9%; Score 34.5; DB 2; Length 512;
 Best Local Similarity 53.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 DAHKSEVAHR-FK 12
 Db 311 BGHKPSIAHDFK 323

RESULT 45
 activin receptor isoform IB3 - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: A40829 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
 R;Rattisano, L.; Wrama, J.L.; Cheifetz, S.; Massague, J.
 Cell 68, 97-108, 1992
 A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate
 A;Reference number: A40829; MUID:92119722; PMID:1310075
 A;Accession: A40829
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-536 <ATT>
 A;Cross-references: GB:MB4120; NID:9191668; PIDN:AAA37172.1; PID:9191669
 A;Experimental source: Balb/c 3T3
 A;Note: sequence inconsistent with the nucleotide translation
 A;Keywords: ATP; receptor kinase homology <KIN>
 Query Match 53.9%; Score 34.5; DB 2; Length 536;
 Best Local Similarity 53.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 C;Superfamily: activin receptor II; protein kinase homology <KIN>
 F;188-487/Binding site: carbohydrate (Asn) (covalent) #status predicted
 R;Attisano, L.; Wrama, J.L.; Cheifetz, S.; Massague, J.
 Cell 68, 97-108, 1992
 A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate
 A;Reference number: A40829; MUID:92119722; PMID:1310075
 A;Accession: C40829
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-528 <ATT>
 A;Experimental source: Balb/c 3T3
 A;Note: sequence inconsistent with the nucleotide translation
 A;Keywords: ATP; activin receptor II; protein kinase homology <KIN>
 F;204-501/Domain: protein kinase homology <KIN>
 Query Match 53.9%; Score 34.5; DB 2; Length 513;
 Best Local Similarity 53.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 DAHKSEVAHR-FK 12
 Db 327 BGHKPSIAHDFK 339

RESULT 46
 activin receptor isoform IB3 - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: C40829 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
 R;Attisano, L.; Wrama, J.L.; Cheifetz, S.; Massague, J.
 Cell 68, 97-108, 1992
 A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate
 A;Reference number: A40829; MUID:92119722; PMID:1310075
 A;Accession: C40829
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-528 <ATT>
 A;Experimental source: Balb/c 3T3
 A;Note: sequence extracted from NCBI backbone (NCBIN:88360; NCBIPI:88361)
 C;Keywords: ATP; receptor kinase homology <KIN>
 Query Match 53.9%; Score 34.5; DB 2; Length 513;
 Best Local Similarity 53.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Do 335 EGHKPSIAHRDFK 347
 RESULT 48
 C14068 polyribonucleotide nucleotidyltransferase (general stress protein 13) BH3347 [imported]
 C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: C84068
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: AB3650; MUID:20512582; PMID:11058132
 A;Accession: C84068
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <STO>
 A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07066.1; GSPDB:GNOC
 A;Experimental source: strain C-125
 A;Genetics:
 A;Name: BH3347
 C;Superfamily: polyribonucleotide nucleotidyltransferase homolog yabR
 Query Match Score 53.1%; Score 34; DB 2; Length 158;
 Best Local Similarity 77.8%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 HKSEVAHRF 11
 Db 35 HISLEVANGF 43
 RESULT 49
 T49921 ribosomal protein-like - *Arabidopsis thaliana*.
 N;Alternate name: protein F17I14.40
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
 C;Accession: T49921
 R;Levan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A.; Reference number: 224490
 A;Accession: T49921
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-156 <BEV>
 A;Cross-references: EMBL:AL233994; GSPDB:GN00063; ATSP:F17I14.40
 A;Experimental source: cultivar Columbia; BAC clone F17I14
 A;Genetics:
 A;Name: ATSP:F17I14.40
 A;Map position: 5
 A;Introns: 19/2; 37/3; 54/3; 85/2; 111/2
 C;Superfamily: *Escherichia coli* ribosomal protein L17
 Query Match Score 53.1%; Score 34; DB 2; Length 156;
 Best Local Similarity 58.3%; Pred. No. 61;
 Matches 7; Conservative 3; Mismatches 0; Indels 2; Gaps 1;
 Qy 3 HK-SEVAHRF 12
 Db 74 HKITTELAHRYK 85
 RESULT 50
 A56125 placental growth factor precursor - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
 C;Accession: A56125
 R;DSalvo, J.; Bayne, M.L.; Conn, G.; Kwok, P.W.; Trivedi, P.G.; Soderman, D.D.; Palisi, J. Biol. Chem. 270, 7712-7723, 1995
 A;Title: Purification and characterization of a naturally occurring vascular endothelial

A;Reference number: A56125; MUID:95221439; PMID:7706320
 A;Accession: A56125
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-158 <DIS>
 A;Cross-references: GB:L40030; NID:g1263413; PIDN:AAA97426.1; PID:g1263414
 C;Keywords: glycoprotein
 Query Match Score 53.1%; Score 34; DB 2; Length 158;
 Best Local Similarity 54.5%; Pred. No. 62;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DAHSEVAHRF 11
 Db 59 DEHNEVEHSHIP 69
 Search completed: April 11, 2003, 15:19:46
 Job time : 18 secs

OM protein - protein search, using sw model

Run on: April 11, 2003, 15:18:37 ; Search time 14 Seconds
 (without alignments)
 52.402 Million cell updates/sec

Title: US-09-846-347-1
Perfect score: 64
Sequence: 1 DAHKSEVAHRFK 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 75 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaas/US08 NEW PUB.PEP:*

2: /cgn2_6/ptodata/2/pubpaas/PCT NEW PUB.PEP:*

3: /cgn2_6/ptodata/2/pubpaas/US06 NEW PUB.PEP:*

4: /cgn2_6/ptodata/2/pubpaas/US05 PUBCOMB.PEP:*

5: /cgn2_6/ptodata/2/pubpaas/US07 NEW PUB.PEP:*

6: /cgn2_6/ptodata/2/pubpaas/US07 PUBCOMB.PEP:*

7: /cgn2_6/ptodata/2/pubpaas/PUBCOMB.PEP:*

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10: /cgn2_6/ptodata/2/pubpaas/US09 PUBCOMB.PEP:*

11: /cgn2_6/ptodata/2/pubpaas/US10 NEW PUB.PEP:*

12: /cgn2_6/ptodata/2/pubpaas/US10 PUBCOMB.PEP:*

13: /cgn2_6/ptodata/2/pubpaas/US60 NEW PUB.PEP:*

14: /cgn2_6/ptodata/2/pubpaas/US60 PUBCOMB.PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
SUMMARIES				
1	64	100.0	12 9	Sequence 1, Appli
2	64	100.0	12 9	Sequence 2, Appli
3	64	100.0	12 9	Sequence 3, Appli
4	64	100.0	13 9	Sequence 4, Appli
5	64	100.0	17 9	Sequence 5, Appli
6	64	100.0	24 9	Sequence 6, Appli
7	64	100.0	26 9	Sequence 7, Appli
8	64	100.0	195 9	Sequence 8, Appli
9	64	100.0	241 9	Sequence 9, Appli
10	64	100.0	268 9	Sequence 10, Appli
11	64	100.0	585 10	Sequence 11, Appli
12	64	100.0	585 12	Sequence 12, Appli
13	64	100.0	609 12	Sequence 13, Appli
14	64	100.0	609 12	Sequence 14, Appli
15	64	100.0	610 9	Sequence 15, Appli
16	64	100.0	610 9	Sequence 16, Appli
17	64	100.0	9 US-10-237-871-2	Sequence 17, Appli
18	64	100.0	10 US-09-984-186-2	Sequence 18, Appli
19	100.0	651 12	US-10-153-064-133	Sequence 19, Appli
ALIGNMENTS				
20	64	100.0	652 12	US-10-153-064-96
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22	64	100.0	652 12	US-10-153-064-105
23	64	100.0	652 12	US-10-153-064-132
24	64	100.0	653 12	US-10-153-064-131
25	64	100.0	655 12	US-10-153-064-130
26	64	100.0	660 12	US-10-153-064-90
27	64	100.0	660 12	US-10-153-064-93
28	64	100.0	668 12	US-10-153-064-102
29	64	100.0	676 12	US-10-153-064-95
30	64	100.0	676 12	US-10-153-064-98
31	64	100.0	676 12	US-10-153-064-101
32	64	100.0	676 12	US-10-153-064-104
33	64	100.0	676 12	US-10-153-064-129
34	64	100.0	677 12	US-10-153-064-125
35	64	100.0	680 12	US-10-153-064-123
36	64	100.0	684 12	US-10-153-064-92
37	64	100.0	692 12	US-10-153-064-101
38	64	100.0	787 9	US-10-237-667-16
39	64	100.0	787 9	US-10-237-871-16
40	64	100.0	787 9	US-10-237-871-16
41	64	100.0	787 9	US-09-984-186-16
42	64	100.0	788 9	US-10-073-118-26
43	64	100.0	788 9	US-10-073-118-26
44	64	100.0	1184 12	US-10-153-064-89
45	64	100.0	604 9	US-10-045-170-01
46	59	92.2	608 9	US-10-165-603-24
47	59	92.2	608 9	US-10-165-603-25
48	59	90.6	11 9	US-09-845-726-1
49	58	90.6	11 9	US-10-076-071-4
50	54	84.4	10 9	US-10-076-071-5
51	51	79.7	195 9	US-10-074-956-23
52	51	79.7	241 9	US-10-074-956-29
53	53	75.0	10 10	US-09-850-373-7
54	54	67.2	534 10	US-09-912-724-4
55	40	62.5	1121 10	US-09-970-711-28
56	37	57.8	535 10	US-09-312-762A-14
57	36	56.2	535 10	US-09-731-118-41
58	36	56.2	15 9	US-10-073-118-40
59	36	56.2	28 9	US-10-073-118-39
60	36	56.2	30 9	US-10-073-118-39
61	36	56.2	145 10	US-09-922-995-2
62	36	56.2	330 9	US-09-738-626-4874
63	36	56.2	330 9	US-09-746-660A-86
64	36	56.2	537 9	US-10-047-542-74
65	35	54.7	55 10	US-09-864-761-40232
66	35	54.7	140 9	US-09-791-932-93
67	35	54.7	313 9	US-10-029-180-4
68	35	54.7	657 10	US-09-833-745-36
69	35	54.7	657 10	US-09-833-745-37
70	35	54.7	1295 9	US-09-789-390-30
71	35	54.7	1295 9	US-09-789-390-32
72	35	54.7	1295 9	US-09-789-390-34
73	35	54.7	1295 9	US-09-789-390-37
74	35	54.7	1295 9	US-09-789-390-39
75	35	54.7	1303 9	US-09-789-390-39

RESULT 1
 US-09-846-347-1
 ; Sequence 1, Application US/09846347
 ; Publication No. US2003040602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKONSKI, George
 ; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
 ; FILE REFERENCE: 2132-032
 ; CURRENT APPLICATION NUMBER: US/09-846,347
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 1
 ; 1999-04-14


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; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1949 DALTONS
; FILE REFERENCE: 2132.047
; CURRENT APPLICATION NUMBER: US/09/845,727
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 8
US-10-074-956-24
Sequence 24, Application US/10074956
Publication No. US2002019332A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 6
US-09-846-328-1
Sequence 1, Application US/09846328
PATENT NO. US2002160531A1
GENERAL INFORMATION:
APPLICANT: JACKOWSKI, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
FILE REFERENCE: 2132.051
CURRENT APPLICATION NUMBER: US/09/846,328
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 9
US-10-074-956-27
Sequence 27, Application US/10074956
Publication No. US2002019332A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 7
US-09-846-329-1
Sequence 1, Application US/09846329
PATENT NO. US2002161177A1
GENERAL INFORMATION:
APPLICANT: JACKOWSKI, George
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular
TITLE OF INVENTION: Of 2937 Dalton
FILE REFERENCE: 2132.052
CURRENT APPLICATION NUMBER: US/09/846,329
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 10
US-10-074-956-28
Sequence 28, Application US/10074956
Publication No. US2002019332A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10

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Query Match 100.0%; Score 64; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 1 DAHKSEVAHRFK 12

Query Match 100.0%; Score 64; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 1 DAHKSEVAHRFK 12

Query Match 100.0%; Score 64; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00015; Length 195;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 1 DAHKSEVAHRFK 12

Query Match 100.0%; Score 64; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.0002; Length 241;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 25 DAHKSEVAHRFK 36

Query Match 100.0%; Score 64; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 25 DAHKSEVAHRFK 36

PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 28
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-074-956-28

Query Match Best Local Similarity Score DB Length
; Matches 12; Conservative 100.0%; Pred. No. 0.00053; 268;
; Qy 1 DAHKSEVAHRFK 12
; Db 25 DAHKSEVAHRFK 36

RESULT 11
; -03-929-552-2
; Sequence 2, Application US/09929552
; Patent No. US2002023080A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SEQ ID NO: 5
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-153-064-5

Query Match Best Local Similarity Score DB Length
; Matches 12; Conservative 100.0%; Pred. No. 0.00053; 0;
; Qy 1 DAHKSEVAHRFK 12
; Db 1 DAHKSEVAHRFK 12

RESULT 13
; US-10-153-064-7
; Sequence 7, Application US/10153064
; Patent No. US2002014281A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 7
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-153-064-7

Query Match Best Local Similarity Score DB Length
; Matches 12; Conservative 100.0%; Pred. No. 0.00055; 609;
; Qy 1 DAHKSEVAHRFK 12
; Db 25 DAHKSEVAHRFK 36

RESULT 14
; US-10-237-667-2
; Sequence 2, Application US/10237667
; Publication No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittot, Jean-Dominique
; Yeh, Patrice
; Jung, Gerard
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:

Query Match Best Local Similarity Score DB Length
; Matches 12; Conservative 100.0%; Pred. No. 0.00053; 585;
; Qy 1 DAHKSEVAHRFK 12
; Db 1 DAHKSEVAHRFK 12

Query Match Best Local Similarity Score DB Length
; Matches 12; Conservative 100.0%; Pred. No. 0.00053; 0;
; Qy 1 DAHKSEVAHRFK 12
; Db 1 DAHKSEVAHRFK 12

STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,667
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-Jan-1997
 APPLICATION NUMBER: US 08/255,927
 FILING DATE: 28-Jul-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-Jan-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-Jan-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3808
 TELEFAX: (610) 454-3839

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-237-667-2

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

US-10-237-708-2

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

US-10-237-708-2

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

US-10-237-708-2

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

US-10-237-708-2

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

US-10-237-708-2

Query Match 100.0%; Score 64; DB 9; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.00055; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 ||||| | | | |
 Db 25 DAHKSEVAHRFK 36

US-10-237-708-2

RESULT 16
 US-10-237-866-2
 ; Sequence 2, Application US/10237866
 Publication No. US20030036171A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guittot, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice
 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,866
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-Jan-1997
 APPLICATION NUMBER: US 08/255,927

FILING DATE: 31-Jan-1997
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 28-Jul-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-Jan-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-Jan-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3808
 TELEFAX: (610) 454-3839

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-237-708-2

FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38, 619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3808
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2;
SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-871-2

Query Match 100.0%; Score 64; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.00055; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Db 25 DAHSEVAHRFK 36

MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-871-2

Query Match 100.0%; Score 64; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.00055; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Db 25 DAHSEVAHRFK 36

RESULT 18
US-09-984-186-2
; Sequence 2, Application US/09984186
; Patent No. US2002015101A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guittton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,871
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38, 619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2;
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-237-871-2

RESULT 18
US-09-984-186-2
; Sequence 2, Application US/09984186
; Patent No. US2002015101A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guittton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-OCT-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38, 619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2;
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-984-186-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2;

Patent No. US20020142814A1
GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

RESULT 19
US-10-153-064-133

; Sequence 133, Application US/10153064
; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.

TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins

FILE REFERENCE: PF556

CURRENT FILING NUMBER: US/10/153,064

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/293,212

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: PatentIn version 3.1

SEQ ID NO 99

LENGTH: 652

TYPE: PRT

ORGANISM: Homo sapiens

US-10-153-064-99

; Sequence 99, Application US/10153064

; Patent No. US20020142814A1

; GENERAL INFORMATION:

APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT FILING NUMBER: US/10/153,064
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 652
TYPE: PRT
ORGANISM: Homo sapiens

US-10-153-064-132

Query Match 100.0%; Score 64; DB 12; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
 Db 68 DAHKSEVAHRFK 79

RESULT 24

US-10-153-064-131
 ; Sequence 131 Application US/10153064
 ; Patent No. US20020142814A1

; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PFS56
 ; CURRENT APPLICATION NUMBER: US/10/153,064

; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/293,212

; SOFTWARE: PatentIn version 3.1

; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 90

; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-153-064-90
 ; Sequence 90 Application US/10153064

; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PFS56
 ; CURRENT APPLICATION NUMBER: US/10/153,064

; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/293,212

; SOFTWARE: PatentIn version 3.1

; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 90

; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-153-064-131
 ; Sequence 131 Application US/10153064

; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PFS56
 ; CURRENT APPLICATION NUMBER: US/10/153,064

; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/293,212

; SOFTWARE: PatentIn version 3.1

; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 90

; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-153-064-131
 ; Sequence 131 Application US/10153064

; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PFS56
 ; CURRENT APPLICATION NUMBER: US/10/153,064

; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/293,212

; SOFTWARE: PatentIn version 3.1

; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 90

; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-153-064-130
 ; Sequence 130 Application US/10153064

; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PFS56
 ; CURRENT APPLICATION NUMBER: US/10/153,064

; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/293,212

; SOFTWARE: PatentIn version 3.1

; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 90

; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-153-064-90
 ; Sequence 90 Application US/10153064

; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PFS56
 ; CURRENT APPLICATION NUMBER: US/10/153,064

; CURRENT FILING DATE: 2002-05-24
 ; PRIORITY FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/293,212

; SOFTWARE: PatentIn version 3.1

; NUMBER OF SEQ ID NOS: 137
 ; SEQ ID NO 90

; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

```

; NAME/KEY: SITE
; LOCATION: (561)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-153-064-102

Query Match
Best Local Similarity 100.0%; Score 64; DB 12; Length 668;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 83 DAHKSEVAHRFK 94

RESULT 29
US-10-153-064-95
; Sequence 95, Application US/10153064
; Patent No. US20020142814A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153, 064
CURRENT FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: 60/293, 212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
LENGTH: 676
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-064-95

Query Match
Best Local Similarity 100.0%; Score 64; DB 12; Length 676;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 91 DAHKSEVAHRFK 102

RESULT 30
US-10-153-064-98
; Sequence 98, Application US/10153064
; Patent No. US20020142814A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153, 064
CURRENT FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: 60/293, 212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 98
LENGTH: 676
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-064-98

Query Match
Best Local Similarity 100.0%; Score 64; DB 12; Length 676;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 91 DAHKSEVAHRFK 102

RESULT 31
US-10-153-064-99
; Sequence 99, Application US/10153064
; Patent No. US20020142814A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153, 064
CURRENT FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: 60/293, 212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 676
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-064-99

Query Match
Best Local Similarity 100.0%; Score 64; DB 12; Length 676;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 91 DAHKSEVAHRFK 102

RESULT 32
US-10-153-064-104
; Sequence 104, Application US/10153064
; Patent No. US20020142814A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153, 064
CURRENT FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: 60/293, 212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 676
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-064-104

Query Match
Best Local Similarity 100.0%; Score 64; DB 12; Length 676;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 91 DAHKSEVAHRFK 102

RESULT 33
US-10-153-064-129
; Sequence 129, Application US/10153064
; Patent No. US20020142814A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153, 064
CURRENT FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: 60/293, 212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 129
LENGTH: 676

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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-064-129

Query Match 100.0%; Score 64; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 0.00052; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 92 DAHKSEVAHRFK 103

RESULT 34
US-10-153-064-125
; Sequence 125, Application US/10153064
; Patent No. US20020142814A1

; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 677
; ORGANISM: Homo sapiens
; US-10-153-064-125

RESULT 35
US-10-153-064-123
; Sequence 123, Application US/10153064
; Patent No. US20020142814A1

; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 677
; ORGANISM: Homo sapiens
; US-10-153-064-123

RESULT 36
US-10-153-064-122
; Sequence 122, Application US/10153064
; Patent No. US20020142814A1

; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 677
; ORGANISM: Homo sapiens
; US-10-153-064-122

RESULT 37
US-10-153-064-101
; Sequence 101, Application US/10153064
; Patent No. US20020142814A1

; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,064
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (585)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-10-153-064-101

Query Match 100.0%; Score 64; DB 12; Length 692;
Best Local Similarity 100.0%; Pred. No. 0.00064; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFK 12
Db 107 DAHKSEVAHRFK 118

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-064-101

RESULT 38
US-10-237-667-16
; Sequence 16, Application US/10237667
; Publication No. US20030022308A1

; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittot, Jean-Dominique
; Jung, Gerard
; Yen, Patrice

; TITLE OF INVENTION: NOVEL BILOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
; US-10-153-064-92
; RESULT 36
; US-10-153-064-92

```

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,708

FILING DATE: 10-SEP-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

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TELEFAX: (610) 454-3808

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3139

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 787 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-237-708-16

Query Match

Best Local Similarity 100.0%; Pred. No. 0.00074;

Mismatches 0; Indels 0; Gaps 0;

Sequence 16, Application US/10237866

Publication No. US2003003617A1

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,866

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/237,708

FILING DATE: 10-SEP-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3808

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 787 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-237-708-16

Query Match

Best Local Similarity 100.0%; Pred. No. 0.00074;

Mismatches 12; Conservative 0; Indels 0; Gaps 0;

Sequence 16, Application US/10237866

Publication No. US2003003617A1

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,866

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3808

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 787 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-237-708-16

Query Match

Best Local Similarity 100.0%; Pred. No. 0.00074;

Mismatches 12; Conservative 0; Indels 0; Gaps 0;

Sequence 16, Application US/10237866

Publication No. US2003003617A1

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,866

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3808

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 787 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-237-708-16

Query Match

Best Local Similarity 100.0%; Pred. No. 0.00074;

Mismatches 12; Conservative 0; Indels 0; Gaps 0;

Sequence 16, Application US/10237866

Publication No. US2003003617A1

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,866

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3808

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 787 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-237-708-16

Query Match

Best Local Similarity 100.0%; Pred. No. 0.00074;

Mismatches 12; Conservative 0; Indels 0; Gaps 0;

Sequence 16, Application US/10237866

Publication No. US2003003617A1

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/237,866

FILING DATE: 10-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-JAN-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610

APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US 08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEX/FAX: (610) 454-3839
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 787 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 SOURCE DESCRIPTION: SEQ ID NO: 16:
 US-10-237-866-16

Query Match 100.0%; Score 64; DB 9; Length 787;
 Best Local Similarity 100.0%; Pred. No. 0.00074; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Sequence ID NO: 16:

Qy 1 DAHKSEVAHRFK 12
 Db 203 DAHKSEVAHRFK 214

RESULT 41
 US-10-237-871-16
 Sequence 16, Application US/10237871
 Publication No. US20030036172A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guittton, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice
 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,871
 FILING DATE: 29-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST92006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEX/FAX: (610) 454-3839
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 787 amino acids

RESULT 42
 US-09-984-186-16
 Sequence 16, Application US/09984186
 Patent No. US2002015101A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guittton, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice
 TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/984,186
 FILING DATE: 29-Oct-2001
 CLASSIFICATION: <Unknown>

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-071-S

Query Match 84.4%; Score 54; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 HK\$VAHRRK 12
Db 1 HK\$VAHRFK 10

Search completed: April 11, 2003, 15:20:27
Job time : 16 Secs

